

Figure 1

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Figure 2

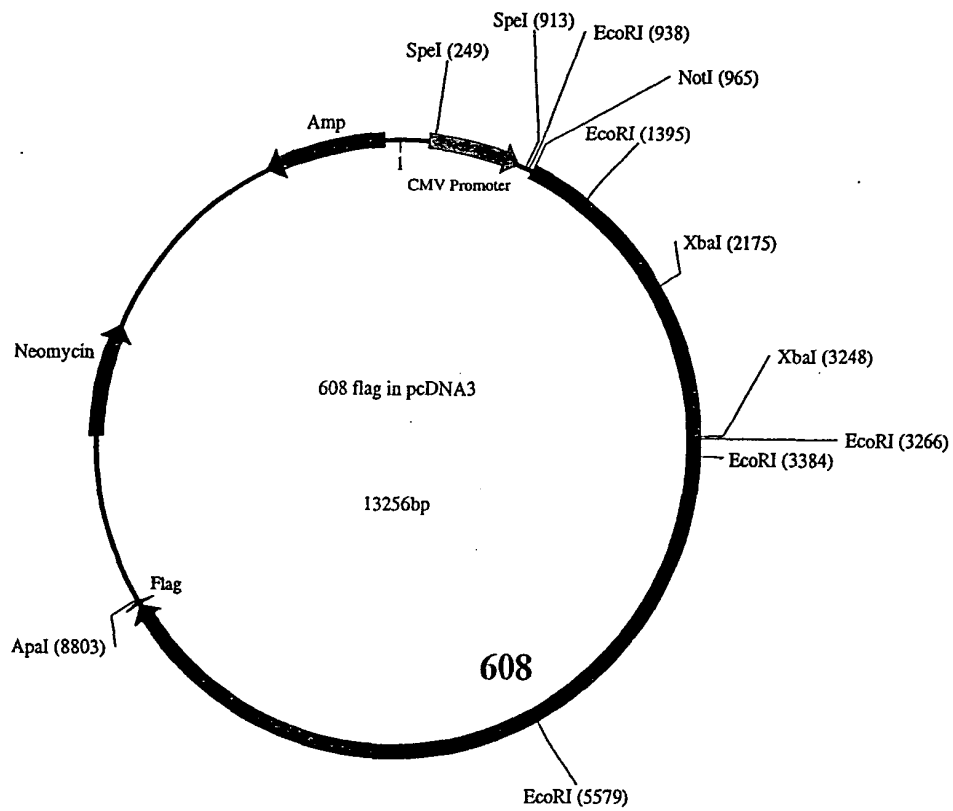


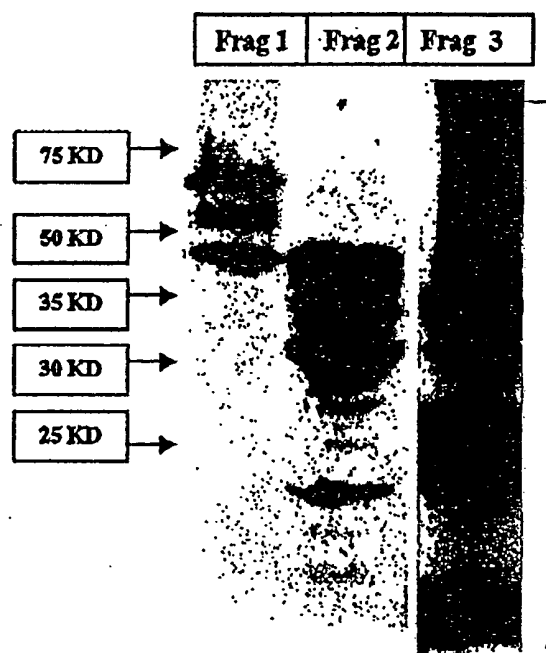
Figure 3

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Figure 4





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Figure 5

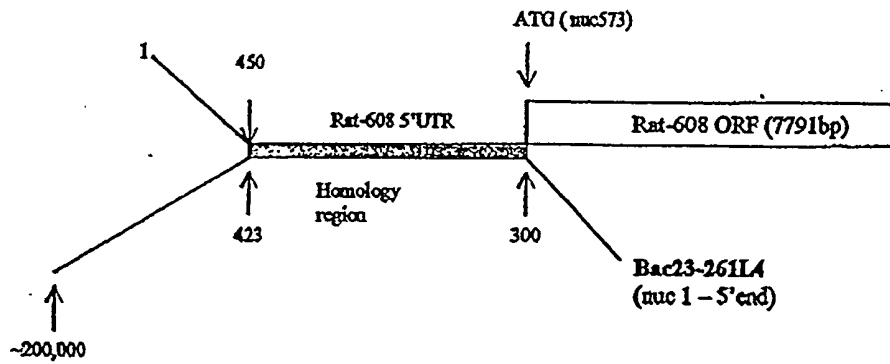
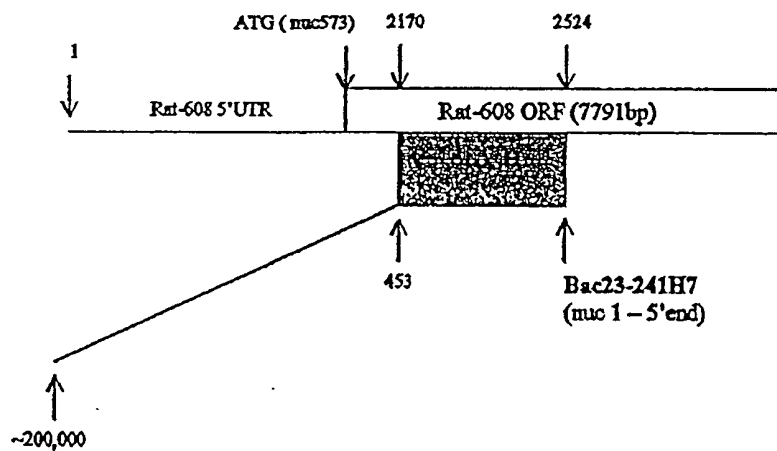


Figure 6



**THE UNIVERSITY OF CHICAGO**

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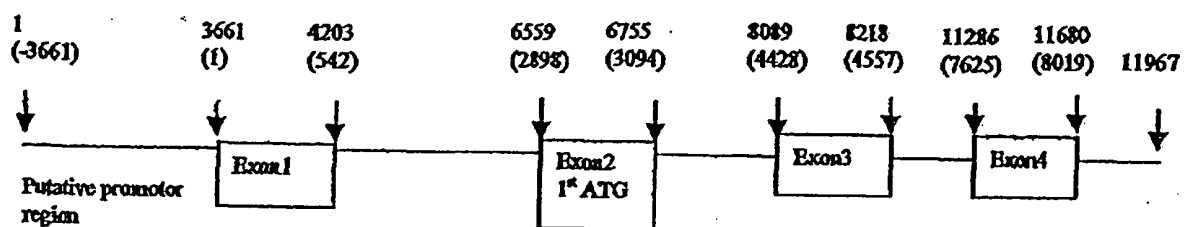
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AAGCAGACGATGGCGGCAGACACTGCAATTCCTGTCCCTGGAAGCACCTGTTCAGAAT  
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Figure 8

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length
1	1	542	542	2356
2	2898	3094	197	1334
3	4428	4557	130	3068
4	7625	8019	394	

Figure 9



[illegible]

cDNA_rat	1	ogagagacgcagaaaggttacggctgcgagaagacgcagaaaggggtccag
genomic_hu	1	-----
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genomic_hu	1	-----
cDNA_rat	101	atgtcacttcagtgcactgaggccaggcaaaaacggcgcggaaggattttgt
genomic_hu	1	-----
cDNA_rat	151	gtagcttgggacccctttcatagacactgatgacacgtttacgcaaaatag
genomic_hu	1	-----
cDNA_rat	201	aaatttgaggagaaaacgcctgggccttcgggaaggagtgattgattagta
genomic_hu	1	-----
cDNA_rat	251	cttgcaagtttaggtgactttaaggagaactaactaatgtatactattga
genomic_hu	1	-----
cDNA_rat	301	gggaggaggaagagcattacagagtttcagcagcagcaggaaagccttg
genomic_hu	1	-----
cDNA_rat	351	gttaatttggaaatggatgatagcattaaataacagaagcgcctccagg
genomic_hu	1	-----
cDNA_rat	401	tototgaagottoagtcccccagctgaagocagaaaagaotaagcccaa
genomic_hu	1	-----
cDNA_rat	451	taagccttttgatccctttggaagcaaagaactttccttcctgggggtga
genomic_hu	1	-----
cDNA_rat	501	agactctcctcagaagatttcctgtctctgcctatgttacaagaggaatc
genomic_hu	1	-----
cDNA_rat	551	aaaaccaagacagaagagctcaggatgcagggtgagaggcaggggaagtcag
genomic_hu	1	-----
cDNA_rat	601	cggtttgttgatctccctcaotgotgtotgootgggtgtcaooctggga
genomic_hu	1	-----
cDNA_rat	651	gcaggggcotgtcctgcgcgtgtgcctgotatgtgccacagaggtgcac
genomic_hu	1	-----
cDNA_rat	701	tgtacatttoggtaacctgacctccatcccagatggcatccgggccaatgt
genomic_hu	1	-----
cDNA_rat	751	ggaacgaataaatttaggatataacagcottaactagattgacagaaaacg
genomic_hu	1	-----
cDNA_rat	801	acotttgatggcctgagcaaacctggagttactcatgotgcacagtaatggc
genomic_hu	1	-----
cDNA_rat	851	attcacagagtcagtgacaagaccttctcgggcttgcagtccttcaggt
genomic_hu	1	-----
cDNA_rat	901	ottaaaaaatgagctataacaaggtccaaatcattoggaaggataottttct
genomic_hu	1	-----

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cDNA_rat genomic_hu	1001	ttcatcaaccctgaggccttttatggacttacctcgctccgcttggtaca
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genomic_hu	1	-----
cDNA_rat	2151	ggcgaatccctaatagacaaaaatgggsagttggaactgcagatggctgac
genomic_hu	1	-----
cDNA_rat	2201	agctttgatgoaggtotttaccactgcataagcaccaatgatgcagatgc
genomic_hu	1	-----
cDNA_rat	2251	ggatgtttcacatacaggataactgtggttagagccctatggagaaagca
genomic_hu	1	-----
cDNA_rat	2301	cacatgacagtgagggtccagcacacagtggttacgggtgagacgctcgao
genomic_hu	1	-----
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genomic_hu	1	-----
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genomic_hu	1	-----

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cDNA_rat	5251	tgagaagggcaaaaggccagcagtaagcatgtccccccacctcagccttc
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genomic_hu	1	-----
cDNA_rat	5351	aagagtgtttttgataagaaacctggtcaaaaoccaaottccaaacatct
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genomic_hu	1	-----
cDNA_rat	6201	tgtatataagaagcatcgtctccttcagtgggggcacttatgagtgcatt
genomic_hu	1	-----
cDNA_rat	6251	gccaccagctcctcaggctcagagagaagggtagtgattccttactgtgga
genomic_hu	1	-----

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c_hu	940	atgtgaGGCTTTCAGATTTCAGCGACTTTATCTGTGTGGcccgaaatgaa
rat	7451	ggaGGAGAGAGTGTGTGGTAGTGCAAGTTAGAAGTCCTAGAAATGCTGAG
c_hu	990	ggtGGAGAGAGCGTGTGGTAGTACAGTTAGAAGTACTGGAATGCTGAG
rat	7501	AAGACCAACATTTCAGAAACCCATTCAACGAAAAagtcatcgcccaagctg
c_hu	1040	AAGACCGACATTTCAGAAATCCATTTAATGAAAAaatagttgccagctgg
rat	7551	gcaagcccgtAGCACTGAACTGCTCTGTGGATGGGAACCCCCACCTGAA
c_hu	1090	gaaagtccacAGCATTGAATTGCTCTGTGTGATGGTAACCCACCACCTGAA
rat	7601	attacCTGGATCTTACCTGACGGCACACAGTTTGCTAACAGACCAcacaa
c_hu	1140	ataatCTGGATTTTACCAAAATGGCACACGATTTTCCAATGGACCAcaaaag
rat	7651	ttccccGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTTACAAAgcaa
c_hu	1190	ttatcagTATCTGATAGCAAGCAATGGTTCTTTTATCATTCTTAAaocaa
rat	7701	ctcggaacaagtCAGGGAAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGC
c_hu	1240	ctcgggaggatgCAGGAAAATATCGCTGTGCAGCTAGGAATAAGTTGGC
rat	7751	TAcatcgagaaactaatcctgttagagATTGGGCAGAAGCCAGTCATTCT
c_hu	1290	TAtattgagaaattagtcattattagaaATTGGCCAGAAGCCAGTTATTCT
rat	7801	GACATACGAAACCAGGGatggtgaagagcgtCAGTGGGGAACCGTTATCAC
c_hu	1340	TACCTATGCACCAGGGAocagtaaaaggoatCAGTGGAGAATCTCTATCAC
rat	7851	TGCATTGTGTGTCTGATGGgATCCCCAAGCCAAATGTCAAAGTGGACTACA
c_hu	1390	TGCATTGTGTGTCTGATGGaATCCCTAAGCCAAATATCAAATGGACTATG
rat	7901	CCGGGTGGccatGTAAATCGACAGGCCTCAAGTGGATGGAAAATACATAct
lc_hu	1440	CCRAAGTGGtlatGTAGTAGACAGGCCTCAAATTAATGGGAAATACATatT
rat	7951	GCATGAAAATGGCAGCGTGGTCATCAAAGCAACAACAGCtcacgaccaAG
c_hu	1490	GCATGACAATGGCACCTTAGTCATTAAAGGAAGCAACAGCttatgacagAG
rat	8001	GAAATTATATCTGTAGGGCTCAAAACAGTGTGGCCAggcagttattago
c_hu	1540	GAAACTATATCTGTAAGGCTCAAAATAGTGTGGTCAatacaotgattact
rat	8051	gtgtCAGTGATGGTTGTGGCCTACCCTCCCCGAATCATAAActacotACC
c_hu	1590	gttcCAGTAATGATTGTAGCCTACCCTCCCCGAATTACAAAtogtccACC
rat	8101	CAGGAACATGCTCAGGAGGACAGGGGAAGGCatgCAGCTCCACTGTGTGG
c_hu	1640	CAGGAGTATTGTCAACAGGACAGGGGCAGCctttCAGCTCCACTGTGTGG
rat	8151	CCTTGGGAATCCCCAAGCCaaAAGTCACCTGGGAGACGCCAAGACACTCC
c_hu	1690	CCTTGGGAGTTCCCCAAGCCagAAATCACATGGGAGATGCCTGACCACTCC
rat	8201	CTGCTCTCAAaagcaacagcaagaaaaaccCATAGAAAGTGAGATGCTTCA
c_hu	1740	CTTCTCTCAAcggcaagtaagagaggacaCATGGAAGTGAGCAGCTTCA
rat	8251	CCCACAAGGTACGCTgGTCAATTCAGAAATCTCCAAACCTCGGATTCCGGag
c_hu	1790	CTTACAAGGTACCCTaGTCAATTCAGAAATCCCCAAACCTCCGATTCTGGga
rat	8301	tcTATAAGTGCAGAGCTCAGAACCTACTTGGgactGATTACGCAACAACT
c_hu	1840	taTACAAATGCACAGCAAAAGAACCCACTTGGtagTGATTATGCAGCAACG
rat	8351	TACATCCAGGTACTCTGACAGGAAGggggagactaaaattcaacagaagt
c_hu	1890	TATATTCAAGTAATCTGACATGAAataataaagtcacaacatctgggca

24/90

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~231 7	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

204020:050455

[illegible]

ATGAAGGTTAAAGGACAGAGGAATCACCTTGCTTGCTGGTCTCCTTTGCTGTGATCTGCCTGGTGCACC  
CCTGGGGGGCAAGGCTGTCTCTCGCCGCTGTGCCTGTTATATGCCTACGGAGGTACACTGCACATTTTCGG  
TACCTGACTTCCATCCAGACAGCATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAACAGCTTG  
GTTAGATTGATGGAACAGATTTTTCTGGCCTGACCAAACCTGGAGTTACTCATGCTTCACAGCAATGGC  
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CACTCCCTTCTCTCAACGGCAAGTAAAGAGAGGACACATGGAAGTGAGCAGCTTCACTTACAAGGTACC  
CTAGTCATTAGAAATCCCCAAACCTCCGATTCTGGGATATACAAATGCACAGCAAAGAACCACCTTGGT  
AGTGATTATGCAGCAACGTATATTCAAGTAATCTGA



Figure 13

A

Region			Region Length	% identity	% positives	% gaps
General	Rat	Human				
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region			% identity	% positives	% gaps
Rat	Mouse	Length			
1-238	1-238	238	91	92	1

C

Region			Region Length	% identity
General	Rat	Human		
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region			Region Length	% identity
General	Rat	Mouse		
1-720	1-718	1-720	720	93

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[illegible]

CGAGAGACGACAGAGAGTTACGGCTGCGAGAAGACGACAGAGGGTCCAGAAAAGGAAA  
CAGAGGGTCCAGGAAA-GGAAA

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CTACTGGAGGGGAGTTGGGACAAAGCGAGCGACCAAGGGACATCGCTTCAGTGACTGAA

GCCAGGCAAAAAGCGGGGAAGGATTTTGTGTAGCTTGGGACCCCTTCATAGCACTGAT  
 -----  
 GCCAGGCAAAAAGGAGGGGAAGGATTATATGTAGCCTGGGAGCGCTTCATAAACACTGAT

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GAGTGTGTTGTGCAAGCAACGCAATTGAGGAGAAACGCTGGGCGTCGGAAGAAGGA

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GTGATCGATTAGTACTTGTAGTTTAGGTGAGTTT--GAGACTAACTAACTATACTA

TTGAGGGGAGGAGGAAAGCATTACAGAGTTTCCAGCAGCAGCAGGAAAGCTTTGGTTAAAT  
TTGAGGGGAGAGGAGAGCATT-----CCAGCAGCAGCAGGAAAGCTTTGGTTAGT

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CCCCAGCTGAAAGCCAGAAAAGACTAAGCCCTAAGCCCTTTTGATCCCTTTGGAAGCA  
-----  
CCCCAGCT-----A-GGTAAAGCCTACTAAGCCCTTTTGCTCCCGTTGGAAGCA

AAGAACTTTCCTTCCCTGGGGTGAAAGACTCTCTCAGAAGATTTCCTGTCTCTGCTATG  
AAGAACGTTCTCTCAATCAGGTGAAGGCTCTCTCAGAAGATTTCCTGTCTCTGCTTATG

TTACAGAGGAATCAAACCAAGACAGAAAGCTCAGGATCGAGGTGAGAGGCAGGGAAG  
ATGAAGGTAAAGGCAGAGGAA  
TTACAGAGGATTCAAAGCAAGACAGAAAGCTCAGGATGCAGAAAGACAGGCAGGGAAG  
\*\*\* \*\* \* \*\* \* \*\* \*

TCAGCGGCTTGTTGATCTCCCTCACTGCTGCTGCGCTGGTGGTCAOCCCTGGGAGCAGGG  
 TCACTGCTTGCTGGGCTCTCCTTGCTGTGATCTGCCCTGGTGGCAOCCCTGGGGGCAGGG  
 TCAGCTGCTGCTGATCTCCCTCACTGCCATCGCCCTGGTGGTCAOCCCTGGGAGCAGGG  
 \*\*\* \* \*\*\*\*\* \* \*\*\*\*\* \* \*\* \*\*\*\*\* \*\*\*\*\* \* \*\*\*\*\*

CCTGTCTCTCGCGCGCTGTGGCGCTATGTGCGCCACAGAGGGTGCACTGTACATTTGGGTACC  
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 TCTGTCTCTCGCGGATGTGGCGCTATGTGCGCCACAGAGGGTGCACTGTACATTTGGGGAAC  
 \*\*\*\*\*  
 \*\*\*\*\*  
 \*\*\*\*\*  
 \*\*\*\*\*

TGACCTCCATCCAGATGG-CATCCGGCCATGTGGAACGATAAATTAGGATATAAC  
 TGACTTCATCCAGACAG-CATCCGCCCAATGTGGAACCATCAATTAGGATACACAC  
 TGACCTCCATCCAGAGGGGCATCCAGCCCATGTGGAACGAGTCAAATTAGGGTATAAC  
 \*\*\*\*\*  
 \*\*\*\*\*  
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AGCCTTACTAGATTGACAGAAAAAGACTTTGATGGCCTGAGCAAACTGGAGTTACTCATG  
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AGCCTCACTAGATTGACAGAAAAATGACTTTCTGGCCTGAGCAGCACTGGAGTTACTCATG  
\*\*\* \* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\* \* \*\*\*\*\* \* \*\*\*\*\* \*

CTGCACAGTAATGGCAATTACACAGAGTCAGTGCACAAGAOCTTCTCGGGCTTGCAAGTCTTTG  
CITCACAGCAATGGCAATTACACAAATCOCTGACAGAOCCTTCTCAGATTTCAGAGGCOCTTG  
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\* \* \* \* \*

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\*\*\*\*\*

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\*\*\* \*\*\*\* \*\* \*

GCCTTTTATGGACTTACCTCGCTCGCCTTGGTACATTAGAAGGAAACCGGCTCACAAG  
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GGCTTTTACGGACTCACCTTGCCTCGCCTTGGTACATTAGAAGGAAACCGGCTGACAAG  
\* \*

CTCCATCCGAGACATTGTCTCAATTAAGCTATCTCCAGATATTTAAACCTCTTTCATT  
CTCCACCCAGATACATTGTCTCTTTGAGCTACCTCCAGATATTTAAATCTCTTTCATT  
CTCCATCCGAGACACATTGTCTCTTTGAGCTATCTCCAGATATTTAAACCTCTTTCATT  
\*\*\*\*\* \*\*

AAGTACCTGTTCTGTCTGATAA C TCGT - GACCTCCCTCCCAAAGA AATGGTCTCCTA  
AAGTTCCTATACTTGTCGATAACTTCCT - GACCTCCCTCCCTCAAGAGATGGTCTCCTA  
AGNAACTGTACTTGTATGATAACTTCATGACCTCCCTCCCAAAGA AATGGTCTCCTC  
\*\*\* \* \* \* \* \*\*

GATGCCAAACCTAGAAAGCCTGTATTTCATGGAAACCCATGGACCTGTGACTGCCATT  
TATGCCTGAAGTAGACAGCCTTTACTGCAATGGAAACCCATGGACCTGTGATTGCCATT  
TATGCCAAACCTAGAAAGCCTTTACTTCATGGAAACCCATGGACCTGTGACTGCCATT  
\*\*\*\*\*

AAAGTGGTGTGCTGAGTGGATGCCAGGGAACCCAGATATAATAAAATGCRAGAAAGACAG  
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\*\*\*\*\* \*\* \*

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TTTCTTTTTTTATARKAGGTATTTTCTCAATTCAATTAGAATGATATCCCCAAAAGTC-

\* \* \* \* \*

GACCCCTTTGCTATGGTACCATCTGGAGCTTTCCATGTACAAAGCCACCATTTGATCCAT  
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 -CCCATAACTCCCOCCCA-----CTTCCCTACCTAACCATTTC--CCATTTTTTGGC  
 \*\* \* \* \* \* \* \*\* \* \* \* \* \*

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 CCGTGAATCAAGAGAGCTGACTATTCTGGAGACAGTAGTCTCTGCTTTCATCTCTCCC  
 CTGGCATTTCCC-----  
 \* \* \*

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AGGCGGACATGGTCTGTAGTATCCAAAGOCATCAAGGACATCACCACTGCATTCACTG  
AAGCTACATGGTCTGAGTATTCAAAGOCCTCAAGGACATCACCATTCATTCACTG

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CTTGGTTAATGCAAGACCAAATTTCCTTG CAGCTGAACAGAACTGCCACCACATTAGTA

CATTACAGATCCAGTTTTCCTACTGATGCTCAAATCGCTTTAOCAGGGCGGAGATGAGAG  
CATTACAGATCCAGTACTCCAGTGATGCTCAAATCACTTTAOCAGAGCAGAGATGAGGC

CGGAGAGACTCAAATGGACATGATCCTGATGATGAACAATCCAACTGGAAAGCACTG  
CAGTGAARACAAATGGACTATGATTTCAAGGGATAACAATACTAAGCTGGAACATACTG

TCTTGGTTGGCGGCACTATTGDOCTGAGCTGTCCAGGCCAAAGGGGACDCTTCAOCTCACT  
TCTTGGTAGGTGGAAOOGTTGGCCTGAAGTGOCCAGGCCAAGGAGACCCCAOCCCAOAG

TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCCTTACGTTAGGAGGATGGGC  
TGGATTGGCTTCTAGCTGATGGAAGTAAAGTGAGAGCCCTTATGTCAGTGAGGATGGAC

GAATCCTAATAGACAAAATGGGAAGTTGGAACTGCAGATGGCTGACAGCTTTGATGCAG  
GGATCCTAATAGACAAAAGTGGAAAATTTGGAACTCCAGATGGCTGATAGTTTTCACACAG

GTCTTTACCTCTGCATAAGCACCATGATGCAGATGCGGATGTTCTCACATACAGGATAA  
GCGTATATCACTGTATAAGCAGCAATTATGATGATGCAGATATTCTCACCTATAGGATAA

CTGTGGTAGAGCCCTATGGAGAAAGCACACATGACAGTGGAGTCCAGCACACAGTGGTTA  
CTGTGGTAGAAACCTTTGGTCGAAGCCTATCAGGAAAATGGGAATCAATCACACAGTTTTCA

CGGGTGAGAGGCTCGACCTTCATGCGCTTTCCACGGGTGTTCCAGATGCTTCTATTAGCT  
TTGGTGAAACACTTGATCTTCATGCGATCTCTACTGGTATCCAGATGCCTCTATTAGCT

GGATTCTTCCAGGGAACACTGTGTTCTCTCAGCATCAAGAGACAGGCAAATTCCTAACA  
GGGTATTTCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAGAGAAAGTTCCTAACA

[illegible]

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ATGGGACCTTAAGATATTACAGGTTACGCCAAAAGATCAAGGTCATTACCAATGTGTGG  
ATGGCACATTAAAGATATTACAGGTCACCCCGAAAGACCAAGGTTATTATCGCTGTGTGG

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CTGCCAACCCATCAGGGGCGGACTTTTCCAGTTTAAAGTTTCAGTTCAAAGAAAGGCG  
CAGCCAACCCATCAGGGGTTGATTTTGTATTTCCAGTTTCAGTCAAGATGAAAGGAC

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AAAGGATGGTTGAGCATGACAGGGAGGAGGTCGATCTGGACTTGGAGAACCCTCC  
AAAGGCCCTTGGAGCATGATGGAGAACAGAGGGATCTGGACTGATGATCCATCCTA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GTGTTTCCCTTAAGCAGCCAGCATCTTTGAACTCTCTGCATCAGCTTTGACAGGGTCAG  
TTGCTCATCTTAAGGAGCCACAGGTCACAACTCCGTACATCTGCTCTGATGGAGGCTG

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AGGCTGGAAAACAAGTCTCCGGTGTACATAGGAAGAACAACTAGAGACTTAATACATC  
AGGTTGGAAAACACACCTCAAGCACAACTAAGAGGCCAACTATCGGGAATTACACTCC

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GGCGGCGTGGGGATTCCACGCTCCGGGGAITCAGGGAGCATAGGAGGCGAGCTCCCTCT  
AGCGAGTGGAGATTCAACACATCGACGTTTATGGGAGAATAGGAGGCATTTCCTCCCT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CTGCTCGGAGAATTGACCCGCAACGCTGGGCGAGCACTTCTAGAAAAAGCCAAAAGAAAT  
CTGCTAGGAGAATTGACCCCAACATTGGGCGGCACTGTTGGAGAAGCTAAAAAGAAATG

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CTGTGCCAAAAAGCAAGAAATACCAAGTAAAGCCAGTGCCACTGGCTGTTCCCTCG  
CTATGCCAGACAAGCGAGAAATACCAAGTGAAGCCACCCAGTGGTCACCCCACTCC

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

TGGAATCACTGACGAGGAAAAGGATGCTCTGGCATGATTCTCCAGATGAAGAATTCA  
CAACATACCTGGTGAAGAGACGATTCTCAGGCATGCTGGCTCTACATGAGGAATTTA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

TGGTTCTGAACCTAAGGCTTCTGGTGTCCAGGAAGGTCACCAACTGCTGACTCTGGAC  
TGGTCCCGCCACTAAGCTTTGAACTTCCAGCAAGGACAGTGAATGCTGACTCCAGAA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CAGTAAATCATGGTTTATGACGAGTATAGCTTCTGGCAGAGAGTCTCAACTGTGAATC  
CAATATCTGATAGTCTATGACAAACATAAATTATGGCAGAGACTCTCGGTTGTGAAT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CACAAACACTACAACTGAGGACCTTCTGATTCTCAATTAATTTAGTGTAAACAAAGGTA  
CACAAATACTACCACTGAGGACCCACAGATTTCAAACTGTCTACTCTATTAAGACTA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CAGCTGTGACAAAGAGTATGAACCCATCCTAGCAAGCAAAATAGAGATACAACCAACC  
CAGCCATGTCAAAGATATTAACCCCAACATGTCAAGCCAAATACAAGGCACCAACATC

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AAAACCCAATCATTAATCTTTCCATC-----AGTAGCTGAATTCGAGATTCTG-CT  
AACATTCTCACTGTCTTTCCACTGCTACTTGGAGCACTGAATTTGAGGACTCTGACA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CAGGCA---GGAAGAGCATCTTCCAAAGTGCCACCCCTGTAACAGGGGGAAACATGGCT  
GAGGGAGAGGGAAGAGAGCATTTCC--AGTA-ACCCCAATAACAGTAAGGACTATGATC

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

ACCTATGGCCATACCAACACATA--TAGTAGCTTTACAGCAAAGCCAGTACAGTCTTGC  
AAGATGNTCAATGTCAANATGCTTAGTAGCACCCACCAAAA-CTATTA-----TTAG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

AGCCATAAATCCAACAGAAAGTTATGGACTCAGATACCTATTACAGGAGTCAGCAGAC  
AGTCAGTAATACCACAAATAGTCAT-----CAGACATCTGTAAGAGAGTGAAGTGAAC

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CTAGCAGTAGTGACATCTCTCTCACACTACTGCAGACCCCTAGCTTCTCCAGTCACCCCTT  
CCAGGCACATCTCTCTCTCTCTCACACTACTCAAACTACTAGCACCTCCAGTTCCTCTT

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CAGGTTCAACACACACTGCTCTCTTATTTTACATTCTAGAAACAAACATACAGGTA  
CAGATCCACACACAGCTGCTCATCTCTAGTTTCCGATCCCTAGANNNAATAGTACAGTTA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

ACTTCCOCTTGTCAGGCACTTGGGAAGAGAGAGGACAAATTTGGAGCAGAGGGAGAGTTA  
ACATCCCGCTGTTCAGAAGCTTTGGGAGGCAGAGGAAAATTGGCGGAGGGGGGGGATTA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

AAAACCACATAGAAACCCAGTTCTCCGAGGCATAGACACAGGACTGTGAGGCCAGCAA  
TCAGCCATATAGAACTCCAGTTCTCCGAGGCATAGATACAGCAITTTTCAAGTCAACAA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

TCAGGGACCTGCTAACAATAATGTGAGCCAAAGTTCCAGCCACAGAGTAACCTGGGATGT  
CCAGAGGTTCTCTGAAAAAGCACTACTGCAITTTCCAGCCACAGTGCTCAATGTGACAT

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GCCACACATGTCTTCCGAGAGGGGCTCAGTGGCTACTGCAGCACTGTCACTTCCAA  
GTCTGTCTGTCTTCCAGGGAGAGGCTCACCCTGCCACAGCAGCAITTTCTTTTCCAA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GTTCACTCCACAGTGGCTCCCAAACTAAATATTTGGGGTCTAGCAGAAAGTCTA  
GTGCTGCTCCATCACTTCCCAAGCTGACATTGCTAGAGTCCATCAGAAGATCTA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CCACTGTGCTCAAGAAACCACTGTTACTATTTAAGGACAAACAAATGTAGTATTGAGA  
CAACTCTAGTCCAGATCCACTATTACTTGTAGAACAAACCAAGTGTAGANNNGAAA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

TAATAACAACCACTACAAATATTTCCGAGGGGAAAGTAACCACTGATTCCTACGGAG  
NNACACACCCCAATAAAATATTCAGGACTNGAAATTTCCCAAGTGAATCCCACTGGTG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CAGCATGACTTCTGCTCCACATCTGTATCCCTGGGGAAATCTCCTGTAGACAATAGTG  
CAGTCATGACATATGCTCCACATCCATACCGTAGGAAAACTCACAAGTAAACGCCA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GTCACCTGAGCATGCTGGGACCATCCAACTGGGAAAGATTCAAGTGGAAACACACACC  
GTTACCCAGTGTGTCTAGACCAATGAAGCTAAAGAGATTCAAGTGATTACATGCTCAC

050433-03402

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TTCCGAGCCCCCTCAGCACCCCTCAATAOCAC-----CAAGCACAATAATTCCTCAAGA  
TTTCAGGTGCTATCAOCCAGCCCAATGACTATTATAGOCATTACAGGTTTTCAGAA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GGAAACTCCCTTGCCACCAGATCTTTGTAATAACCAAGAAGGAGGGGATGTTAAGA  
GGAAATTCCTGGCAACAGAACTTTGTAATAACCAATAACCCAAAGGCAGATTAAAGAA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

ATCCATATCAATTGGTTTACAAAAGAACCCAGCCGCAAGGTTCCCAAAATAGCTCCTC  
ATCACATAAAGTTAGTTTACAAAAAGCACAGCTGTGATGCTTCTTAAACATCTCCTG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TTTTACCCACAG-GTCAGAGTTCCCOCTCAGATTCTACAACCTCTCTTGACAAGTCCGCA  
CTTTACC-ACAGAGACAAAGTTCCCTTTCCATTTCACACACTTTCAACAAAGTGTGATG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CCAGCTCTGTCTACAACAATGGCTGCCACTCGAACACAGGGCACTGAAGTAGTATCAGGT  
CAAAATTCATCTAATACCTTGACTACCGCTCACCACTACGACCAAA--ACACACAA-T

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GCCAGAAGTCTCTCAGCAGGGAAGAGCAGCCCTTCAOCCACTCTCTCCAG-TGCTTCC  
CCTGGAAGTCTTCCACAAAGAGGAGCTTCCCTTC-CCACCCCTTACCCATATGCTTCC

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TAGCACAATAAGCAAGAGATCTAATACATTAACTTCTTGTCAACGGAAACCCCAAGT  
TAGTATTATAAGCAAGAGCTCAAGTACAAAAGCATCATATCAACGCAACAGCAACCGC

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GACAAGTCTACTGCTACTGCTATCTGCTATTATGCTGHAACCCACGACAGATCCAA  
AACAACTCTTACCTTCCCTGCTCTGCTATCTACTTATGAAACCAACAGAGAGATCTAG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

AGAGGCAAAAGACCAATTAAGGGGCTCG--GAAGAACAGAACCAACGCAACACCCAC  
AGCACAAACAATCAAGAGAGGAOCTCAAAAGAGAACAGGACTGACCCAAACATCTC

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CCCCAGGCAGGTTTCTGGCTATAGTGCATCTACTCAGCTCTAACACAGCTGATACCCCCTT  
TCCAGACCAAGGTTCTGGCTTCACTACACCACTGCTATGACNAGCTCTNNGCTCTNN

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GGCTTTCAGTCAITCCCCACGACAGATGATGGTGAAATGTAAGTGCAGTTGCTTATCA  
NGCAITCACTCAITCCCCACGAAACACAACCTGGGATTTCAGGCACATCAGTTTTC

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CTCAACAACTCTCTTCTGGCA---TACTGACTGTTTGAG-AGTAC--AACCAGAC  
TTCAAGAACTCTTAATCTGACAGATGTGATTGAGAACTAGCCCAAGCACTACTCAGAC

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TTTGGGAATACAAACGCTTTGGAAACAGCTTGTGAGCAATCACAGGAGGTACAC  
TTTGAAGAGCAATTTGCTTCTGAACCACTTTGTCCAGCAATCACACCAGGTACAC

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

AGTGAAGAGAGCTCA---GACAC--ACCACCACTCTCTCAGAGTGGGGGCCCCC  
AAGTAGGAAGCAATCATTAGACACTCACCAACCACTTCTTGAAGCAGCTGTACTCT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AGTGCCCACTCCTTCCCCACCTCCTTTTACTAAGGGTGTGTTACAGACAGCAAAGTCAC  
AATGCCAGTTCCCATCTCCCTCCCTTTACTCAGAGCAGTTACTGACAACTGGCGAC

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ATCAGCTTTCCAGATGACGTCAAATAGAGTGGTCACCATATATGAATCTTCAAGGCACAA  
TCCCAITTTCCGGGCTTATGACAAATACAGTGGTCAAGCTGCACGAATCCTCAAGGCACAA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

TACAGATCTGCAGCAACCTCAGCAGAGGTAGCCCAATCCTGAGATCATAACTGGAAC  
TOCNNNNNNNCR--AATGCCAAGTTCA-----CNAATTTGNCAACNNNNACTCNNNN

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CACTGACTCTCCCTCTAAATCTGTTCCATCCACTTCTGTGCCAGCACTAAGGGTAGATAA  
NACTTCATCTACNTCTAATCTGTTACATTTCTACTCCCATGCCAGCACTAACACAGTTAA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AACACAGAAATTTCTAAATGGAAGCCCTCTCCCTGGCCAGACACAAATATCAGCTCAAGTC  
ATCACAGAAATTTCCAAATTAATCCATCTCCCTGGCCAGAAATACCAATTTTGGCCACAAACC

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ATACTCCGAAACCATTTAGAGAGGGCAAAAGGCCAGCAGTAAGCATGTCCCCCACTCAG  
ATACTCAGACATTGCTGAAAAGGCCAAAAGCCAGAGTAAGCATGTTGGCT-ACTACAG

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

-CCTTCCAGAGGCCAGCACTCATGCCCTCACACTGGAATACACAGAGCATGCAGAAAAGA  
GCTGTCCGAGGCCACCACTCTTGTTCAGATTGGGATGGACAGAGAACACAAAGAGA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GTGTTTTTGTATAAGAAACCTGGTCAA-AACC--CAACTTCCAAACATCTGCCCTAAGTCT  
GTGACTTTGTATAAGAAACCAAGTTCAAGAGCAACACACTTCCAACTCCTTCCCTTTGACT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CTCTACCTAAGACTCTATTGAAAAAGCCAGAATAATTGGAGGAAGGCTGCAGCTTTA  
CTTTGTCTAGGTATATATTTGAAAAGCCAGGATAGTTGGAGGAAGGCTGCAGCTTTA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CAGTTCCAGCTAAATTCAGACGTTTTCTTCTGTGAGGCTGTTGGAGAACCACTGCCCA  
CTATTCCAGCTAACTCAGATGCCCTTCTTCCCTGTGAAGCTGTTGGAAATCCCTGCCCA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

TCATCCACTGGACAGAGTTTCATCAGGANTTGAATATCCCAAGGGACACAGAAAGCC  
CCATTCAATTGGACAGAGTNNNNTCAGGACTTGATTTATCTAAGAGGAACAGAAATAGCA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GCTTCCACGTGCTTCCCAATGGCACCTTGTCCATCCAGAGGGTCAGTATTCAGGACGGTG  
GGGTCCAGGTTCTCCCAATGGTACCCCTGTCCATCCAGAGGGTGGAAATTCAGGACCGGG

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GACAGTACCTGTGCTCTGCATTTAATCCACTGGGGCTAGACCAATTTTCACTCTCTTTGT  
GACAGTACTTGTGTTCCGCAATCTGTTGGCAGACCACTTCATGTCACCTTGT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

CTGTGGTTTTTTTACCCGGCAGGATTTTGGACAGACATGTCAGGAGATCACATTTCACT  
CTGTGGTTTCTATCTCTCCAGGATCTGGAGAGACGTACCAAGAGATCACATTTCACT



504570030432

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

TTGGAAGTACTGTGGAAGTAAAGTGCAGAGTGGAGGGTATGCGAGGGCTACGGTTTCCT  
CCGGAAGCACTGTGGAAGTGAAGTGCAGAGCAGAAGGTAGGCGAAGCGCTACAGTTAOCCT

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GGATACTTGCAAAACAAACGGTGGTCTCAGAAAACGGCCAGGGGAAGCAGAAAGGTCTGGG  
GGATTCTTGCAAAACAAACAGTTGTCTCAGAAATCATCCAGGGGAAGTAGGCAGGCTGTGG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

TAACACCTGATGGAACATTGATCATCTATAATCTGAGTCTTTATGATCGTGGTTTTTACA  
TGACGGTTGACGGAACATTGGTCCCTCCACAATCTCAGTATTTATGACCGTGGCTTTTACA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

AGTGTGTGGCCAGCAACCCATCTGGCCAGGATTCAGTGTGGTTAAGATACAGTCATCA  
AATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCAGTGTGGTTAAGATACAGTCATTG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CAGCTCCOCCTGTCTATTAGAGCAAAAGAGGCAAGCCATCGTTGGGGTTTTAGGTGGAA  
CAGCACCACTGTATTCTAGAGCAAAAGAGGCAAGTCATTGTAGGCAGCTTGGGGTGAAG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GTTTGAAACTGCCCTGCACTGCAAAAGGAATCCTCCAGCCTAGTGTTCAGTGGGTCTTT  
GTTTAAACTGCCCTGCACTGCAAAAGGAATCCTCCAGCCTAGTGTTCAGTGGGTCTTT

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

ATGATGGGACTGAATATAAACCATTCGAGTTGACTCATTCAGATTTTTCTGTATCCAA  
CTGATGGCACTGAAGTGAAACCATTCAGTTTACCAATTCAGATTTGTCTTATTTCAA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

ATGGAACTCTGTATATAAGAACATCGCTCCTTCAGTGGGGGCATTATGAGTGCATTG  
ATGGGACTTTGTATATAAGAACATCGCTCCTTCAGAGAGGGGCATTATGAGTGCATTG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CCACCGCTCCTCAGGCTCAGAGAGAGGGGTAGTGATTCTTACTGTGGAGAGGGAGAGA  
CTACAGTTCCACTGGTTCGGAGCGAAGAGTAGTAATGCTTACAATGGAGAGCGAGTGA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CAATCCCGAGATAGAACTGCTCTCAGAAATGGACTGAGGTGAATTTGGGTGAGAAAT  
CCAGCCCCAGGATAGAGCTGCATCCAGAAAGGACTGAAGTGAATTTGGGGACAAAT

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

TACTACTGAAGTGTCTCAGCTACTGGGGATCCAAAGCCTAGATAATCTGGAGGCTGCCAT  
TACTACTGAAGTGTCTCAGCCACTGGGGAGCCCAACCCCAATAATGTGGAGGTTACCAT

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

CCAGGGCTGTCTGACCACTGGCCACAGAAATGGGCGCGGAATCCAGCTCTACCCAAATG  
CCAGGGCTGTGCTGACCACTGG-----GCAGCTGGATCCAGCTCTACCCAAATG

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GATCCTTGGTGGTTGGGTGAGTGAAGGAAAGACGCTGGTGAATCTTATGTGTGGCAA  
GATCCTTGGTTATTTGGATCAGTAACAGAAAGACAGTGGTGTCTACTTGTGTGGCAA

rat\_cDNA  
human\_5+3\_corrected  
mus\_cDNA\_5

GAAACAAAATGGGAGATGACCTAGTCTGATGATGTCCGCTGAGATTGACACCTGCCA  
GAAACAAAATGGGAGATGATCTGATAGTATGATGTCTAGCCTAAGACTGAAACCTGCCA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

AAATTGAACAGAAGCAGTATTTTAAGAAGCAAGTCTCCATGGGAAAGATTTCAGATTG  
AAATTGAACACAGCAGTATTTTAGAAGCAAGTCTCCATGGGAAAGATTTCAGATTG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

ACTGCAAGGCTCTGGCTCCCTGTGCTGAGGTATCTGGAGTTTGCTGATGGACAG  
ATTGCAAGCTTCCGGCTCCCAAGTCCAGAGATATCTTGAGTTTGCTGATGGAAOCA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TGCTCAACAATGTAGCCCAAGCTGATGACAGTGGCTATAGGACCAAGAGGTACACCTTT  
TGATCAACAATGCAATGCAAGCGATGACAGTGGCCACAGGACTAGGAGATATACCTTT

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TCCACAATGGAACTTTGATTTCAACAAGCTTGGGATGGCAGGAAAGGATATATCT  
TCAACAATGGAACTTTGATTTCAACAAGCTTGGGATGGCAGGAAAGGATATATCTT

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GCTCTGCCAGAACACCTTAGGGAAGATGAGATGAATGTCACCTAACAGTTCTAACAG  
GCTATGCCAGAACACCTTAGGGAAGATGAATGAAGTCCACTTAACAGTTATAACAG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CCATCCACGGATAAGGCAAGCTACAAGACCAATGAGGCTCAGGGCTGGAGAACAG  
CTGCTCCCGGATAAGGCAAGTAAACAAACCAACAGAGAAATCAAGCTGGAGACACAG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CTGTCTTGACTGCGAGGTCACTGGGGAAACGAGCCCAATGATTTTGGTTGCTGCCTT  
CTGTCTTGACTGCGAGGTCACTGGGGATCCCAACCAAAATATTTTGGTTGCTGCCTT

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CCAACAATGTCTTTCTTCTCCAATGACAGTTCACTTTCTATGCCAATAGACTTTGT  
CCAATGACATGATTTCTTCTCCATGATAGGTACAGATTTCTATGCCAATGGGTCTTTGA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

CCATCCATAAAGTGAAACACTTGACTCTGGGGACTATGTGTGCGTAGCTCAGATCTTA  
CCATCAACAAAGTGAAACTGCTGATTTCTGGAGAGTACGTATGTGTAGCCGAAATCCCA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GTGGGATGACACTAAGACATACAACTGGACATTTCTCTTAACCTCCATTATCAATG  
GTGGGATGACACCAAAATGTACAACTGGATGTGGTCTCTAAACCTCCATTATCAATG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

GCCTGTATGCRAACAAGACTGTTATTAAGCCACAGCATTCGGCACTCCAAAATACT  
GTCTGTATACAAACAGACTGTTATTAAGCCACAGCTGTGAGACATTCAAAATACT

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TTGACTGCAGAGCAGATGGGATCCATCTTCCAGGTCAGTGGATTATGCCAGGCAATA  
TTGACTGCAGAGCTGAAGGGACACCATCTCTGAAGTCATGTGGATCATGCCAGCAATA

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

TTTTCCTCCAGCTCCATCTTTTGAAGCAGAGTCAAGGTCATCCAAATGGAACTTGG  
TTTTCCTCAGAGCCCATCTATGGAAGCAGAAATCAGCTCATATAAAATGGAACTTGG

rat\_cDNA  
human 5+3 corrected  
mus\_cDNA\_5

AGATGAGGAACATCCGCTTCTGACTCTGCGGACTTCACTGTGTGTTCCGAGCGAGG  
AAATTAGGAATGTGAGGCTTTCAGATTCAGCGGACTTATCTGTGTGGCCCAATGAAG

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GAGGAGAGAGTGTGTTGGTAGTGCAAGTAGAAGTCCTAGAAATGCTGAGAGAGCAACAT  
GTGGAGAGAGCGTGTGTTGGTAGTACAGTGTAGAGTACTGGAAATGCTGAGAGAGCCGACAT

TCAGAAACCCATTCAACGAAAAAGTCATGCGCCAGCTGGCAAGCCGGTAGCACTGA  
TTAGAAATCCATTTAATGAAAAATAGTTGCCAGCTGGGAAGTCCACAGCAATTGAATT

GCTCTGTGGATGGGAACCCCCAAGTGAATTAAGTGGATCTTACCTGAAGGCACACAGT  
GCTCTGTTGATGGTAACCAACCACTGAATAATCTGGATTTTACCAATGGCAGACGAT

TTGCTAACAGACCACACAATTCCCGTAICTGATGGCAGGCCAATGGCTCTCTCATCCATT  
TTTCCAATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCCTTTATCATT

ACAAAGCAACTCGGAACAAGTCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCT  
CTAAACAACACTCGGGAGGATGCAGGAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGCT

ACATCGAGAACTCATCTGTTAGAGATTGGGCAGAAAGCCAGTCATTCTGACATACGAAC  
ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAAAGCCAGTTATTCTTACCTATGCAC

CAGGGATGGTGAAGAGCGTCAGTGGGGAACGTTATCACTGCATTGTGTCTGATGGGA  
CAGGGACAGTAAAAGGCATCAGTGGAGAATCTCTATCACTGCATTGTGTCTGATGGAA

TCCCCAGOCAAATGTCAAGTGGACTACACCGGGTGGCCATGTAATCGACAGGOCCTCAAG  
TCCCTAAGCCAAATATCAAATGGACTATGCCAAGTGGTTATGTAGTAGACAGGOCCTCAA

TGGATGGAAATACATACTGCATGAAATGGCAGCTGGTCATCAAGCAACACAGCTC  
TTAATGGGAAATACATATTGCATGACAAATGGCACTTAGTCATTAAAGAAGCAACAGCTT

ACGACCAAGGAATATATCTGTAGGGCTCAAACAGTGTGGCCAGGCAGTTATTAGCG  
ATGACAGAGGAACCTATATCTGTAAGGCTCAAATAGTGTGGTCATACTGATTACTG

TGT CAG TGA TGG TTGT GGC CTA CCG CTC CCG AAT CATA AACT ACG TAC CCAG GAA CAT GC  
 TTCC AGT AAT GAT TGT AGO CTA CCG CTC CCG AAT TACA AAT TGT TCA CCG CGG AGT ATT G

TCAGGAGGACAGGGGAAGCCATGCAGCTCCACTGTGTGGCCTTGGGAATCCCCAAGCCAA  
TCAACAGGACAGGGGCAGCCTTTTCACTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAG

AAGTCACCTGGGAGACGOCAGACACTCCCTGCTCTCAAAGCAACAGCAAGAAAACCC  
AAATCACATGGGAGATGCTGACCACTCCCTTCTCTCAAAGCAAGTAAGAGAGGACAC

ATAGGAAGTGAGATGCTTCACTTACAGGTACGCTGGTCATTGAGAAATCTCCAAACCTCGG  
ATGGAAGTGAGCAGCTTCACTTACAGGTACGCTAGTCATTGAGAAATCTCCAAACCTCGG

[illegible]

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ATTCCGGAGTCTATAAGTGCAGAGCTCAGAACCTACITGGGACTGATTACGCAACAACCT  
ATTCTGGGATATACAAATGCACAGCAAGAACCCACTTGGTAGTGATTATGCAGCAACGT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ACATCCAGGTACTCTGACAGGAAGGGGAGACTAAAATTCAACAGAGTCCACATCCACA  
ATATTCAAGTAATCTGACATGAA-----ATAATAAAGT-CAACAA-----CATCTGGGCA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GGGTTTATTTTGGGAAGAAGTTTAAATCAAAGGCAGCCATAGGCATGTAAATGAGTCTGA  
GAATTTATTTTGGGAAGAAGTTTAAATCAAAGGCAGCCATAGGCATGTAAATGAATTTGA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ATACATTTACAGTATTAAATTTACAATGGACATGCGA--TGA--GACTTGTAAATGAAA  
ATACATTTACAGTATTAAATTTACAATGAACATGCAAAATAAAGGACTTGTAAATTAAT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GCATTGTGAAGTGA--ACCGAGTCTCTG--TGGATCTCAAAGCRAACTCTTAACTTAA  
GCATTATGAAGTGAATGACTGATTTAATTAATGGATCTCAAACCAAACCTTTTAACTTAA

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GGCCTTTGATTTTGGCAACAAATATAACAAACATTAAGAGAGAAAAAATGATCCACTAC  
GGCCTTTTATTTTGGCAACAAATAACAAATAACAA--ACATTGAAACGGTTCATAT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

GAAATAACAAACGGCTAATGCACCTGAATTTCT-CAGTAAAAAGACCTTTCTCTGCTAAC  
AAAATAACAAATGGCTAATGTACCTGAATTTTTCAGTAAAAAA--TGAACCTT-CTAAT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AGTTGCCAGCTGCCTCGTGTCTGTTTCTACCAATGTCAAAACATCGCACACAGGGTGA  
A--CCAGTTGCCTAGTGTCCACCTCTATCAATGTTACAAGCATGGCACTCAG--A

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

ATGGAGTCAACGGGAAGATTAAAGTTTGGGCTCTGTGTAATCTCAATGTACAAATATTC  
ACAGAGACAATGGAAAAATATTAATCTGC-----AATCT--ATGTATAAATATTT

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

TGTCNCTGGTTTATAAACAATTTT-GATAAAACCGAAAAAATAAATAAATAAATAAATAA  
TGT---GGTTTATAAATTTTGTCTAAACCTACAGAAAAATAAG-----

rat\_cDNA  
human\_5+3 corrected  
mus\_cDNA\_5

AAAA  
-----  
-----

(rat\_cDNA: SEQ ID NO:7)  
(human\_5+3 corrected: SEQ ID NO:8)  
(mus\_cDNA\_5: SEQ ID NO:9)

Figure 15

rat	MQVRGREVSGLLISLTAVCLVVTGSRACPRRCACVPTVHCTFRYLTSIPDGI PANVE
human_5+3_corrected	MKVKGRTITCLLVSPAVICLVATPGGKACPRRCACVPTVHCTFRYLTSIPDSIPPNVE
mouse_5_corrected	MQVRGREVSCLLISLTALICLVVTGSRVCPRRACVPTVHCTFRDLTSIPD-GEANVE
rat	RINLGYNLSLRLTENDFDGLSKLELLMLHNSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII
human_5+3_corrected	RINLGYNLSLRLTENDFDGSLTLELLMLHNSNGIHTIPDKTFSDLQALQVLKMSYNKVRL
mouse_5_corrected	RVNLGYNLSLRLTENDFDGSLSKLELLMLHNSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII
rat	RKDTFYGLGSLVRLHLDENNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDTFVSLSYLQ
human_5+3_corrected	QKDTFYGLRSLTRLHLDENNIEFINPEVYGLNFLRLVHLEGNQLTKLHPDTFVSLSYLQ
mouse_5_corrected	EKDTLYGLRSLTRLHLDENNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQ
rat	IEKTSFIKYLFLSDNFLTSLPKEMVSYMPNLESYLHGNWTCDCHLKWLSEWMOGNPDI
human_5+3_corrected	IEKTSFIKFLYLSNFLTSLPQEMVSYMPDLDSYLHGNWTCDCHLKWLSDWTQ--PDV
mouse_5_corrected	IEKTSFIKLYLYDNF-TSLPKEMVSSMPNLESYLHGNWTCDCHLKWLSEWMOGNP--
rat	IKCKKDRSSSSPQOCPLCMNPRI SKGRPFAMVPSGAFLCTKPTIDPSLKSKSLVTOEDNG
human_5+3_corrected	IKCKKDRSPSSAQOCPLCMNPRTSKGKPLAMVSAAFQCAKPTIDSSLKSKSLTILEDSS
mouse_5_corrected	-----
rat	SASTSPQDFIEPFGSLSLNMTXXSGNKADMVCSIQKPSRTSPATFEENDYIMLNASFST
human_5+3_corrected	SAFISPOGFMAPFGSLTAMTQSGNEANMVCSIQKPSRTSPATFEENDYIVLNTSPST
mouse_5_corrected	-----
rat	NLVCSVDYNIQPVWQLLALYSDSLILERKPOLITETPSLSRYKQVALRPEDIFTSIEA
human_5+3_corrected	FLVCNIDYGHQPVWQILALYSDSLILERSHLLSETPOLYKYKQVAPKPEDIFTNIEA
mouse_5_corrected	-----
rat	DVRADFFWFQGEKIVLQNRATTLSTLIQIESTDAQIALPRAEMRAERLKWTHIMMNN
human_5+3_corrected	DLRADPSWIMQDQISLQLNRTATTFSTLIQYSSDAQITLPAEMRPVKHFTMI SRDNN
mouse_5_corrected	-----
rat	PKLERTVLVGGTIALSCPGKGDPSFHEWLLADGSKVRAPYVSEDGRILIDKNGKLELQM
human_5+3_corrected	TKLEHTVLVGGTFVGLNCPGQGDPTFHVWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
mouse_5_corrected	-----
rat	ADSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVIGETLDLPCSTGV
human_5+3_corrected	ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIEHTVFIGETLDLPCSTGI
mouse_5_corrected	-----
rat	PDASISWILPGNTVFSQPSRDRQILNNGTLRILQVTPKQGHYQCVANPBGADFSSFKV
human_5+3_corrected	PDASISWVPGNNVLYQSSRDKVLLNNGTLRILQVTPKQGYTRCVANPSGVDFLIPOV
mouse_5_corrected	-----
rat	SVQKKQRMVYEHDRAGGSGLGEPMSSVSLKQPASLKL SASALTGSEAGQVSGVHRKXK
human_5+3_corrected	SVKMKQRFLEHDGETEGSGLDESNPILAKKEPPGAQLRTSALMEAEVGHKHTSTSKRHN
mouse_5_corrected	-----
rat	HRDLIHRRGDSTLRREFRHRQLPLSARRIDPQWALLESKAKXNSVPPKQENTTVKPV
human_5+3_corrected	YRELTLQRRGDSTHRRFENRKHFPSSARRIDPQWALLESKAKKNAMPKRENTTVSPF
mouse_5_corrected	-----

204630-034630

```

rat      PLAVPLVELTDEEKQASGMIPDDEEFMLVLTAKSGVPGRSPTADSGPVNHGFMTSIASGT
human_5+3_corrected PVTTLQLENIPGEEEDSSQMLAEFEFMVPAKKAENLPARTVTADSRITISDPMTNINYGT
mouse_5_corrected  -----

```

```

rat      EVS-TVNPQTLLQSEHLPDFKFLPSVTNGTAVTKSMNPNSLASKIEDTTNQNPIIIFP--SV
human_5+3_corrected EFSPVVSQILLPPEEPTDFKLSTAIKTAMSKNINPTMSSQIQGTTNQHSSTVFPLLGA
mouse_5_corrected  -----

```

```

rat      ARIKSAQAGRAS--SQSAHPVTGGMATYGHNTYSSFTSKASTVLPINPTESYGPQI
human_5+3_corrected  TEFQDSQDMGRGREGHFQSRPPITVRLMIKQNVNKLSSSTNKL--LLESVNTTNSH--QT
mouse_5_corrected

```

```

rat      PITGV6RPSSSDISSHTTADP8FS6HPSGSHTTAS5LFHIPNNNTGNFPLSRHLGRRT
human_5+3_corrected SVREVSEPRNHFYSHTTQILSTSTFPSPDPTAHSQFPIPRNS-TVNIPLFRFGRORK
mouse_5_corrected

```

```

rat      IWSRGVKNFPHRTFVLLRRHRHRTVRLPAIKGPANKNVSVQVPATEYPMCHTCSAEGLTVA
human_5+3_corrected  IGGRGRIISPYRTFVLLRRHRYSIFRSTTIGSSEKSTTAFSATVNLVNTCLSLPRRLTIA
mouse_5_corrected    -----

```

```

rat      TAALSVPSSSHSALPKTNNGVIAEESTTVVKKPELLLFKQAVDIEIITMTTKYSGGES
human_5+3_corrected TAALSFPSSAAPITFPKADIARVPSEESTTLVQNPLLLLENKCP--SVEKTTPTIKYFRTFI
mouse_5_corrected    -----

```

```

      rat      NHVITEASMTSAPTISVSLGKSPVDNSGHLMPGTIQTKDSVETTPLPSPPLSTP--SIP
human_5+3_corrected SQVTPTGAVMTIYAPTISIMEKTHKVNASYPRVSSIMEAKRDSVITSSLSGAIKTPPMTHI
mouse_5_corrected

```

rat TSTKFSKRKTPFLHQIFVNNOKKEGMLKNPYQFGIQQNPAAKLEKPLAPLLPTGQSSPSDST  
 human\_5+3\_corrected AITFPRRRKIPWQQNIFVNNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRSSPFHFT  
 mouse\_5\_corrected

rat TLLTSFPPALSTTMAATONKGTTEVVSAGARSLSAGKKQ-PFTNSSPVLPTSTIKRSNTINF  
 human\_5+3\_corrected TLTSTVMQIPSTNLTAHHHTTKTHNG-SLPT-KKELEFPPLNFMPLPSISKDSSTKS I  
 mouse\_5\_corrected

```

rat          LSTETPT-VTSPATASVIMSETQRTSRKEAKDQIKG-P-RNRNNANTTPQVSGYSAY
human_5+3_corrected ISTQTALPATTPFPAGVITYETQTRSRAQTQREQEPQKHRTDPNISPDQSSGFTTP
mouse_5_corrected  -----

```

```

rat      SALTTADTPLAFSHSPRODDGCVSAVAYHSTTS--LIAITELFKYQTLGNTTALETT
human_5+3_corrected  TAMTP--PALAFTHSPPEHTTGISSTISFESRTINLTDVIELAQASTQTLKSTIASETT
mouse_5_corrected    -----

```

rat                   LLSKSQESTTVKRAS-DTP-FPLLSSGAPPVPTSPPPPTKGVVTDKAVTSAFQMTSNRV  
 human\_5+3\_corrected LSSKSHQSTTTKRASLDTPPIPPFLSSSATIMPVPIISFFPTQRAVTDTRGSDSHFRIMTNTV  
 mouse\_5\_corrected

```

rat      VTIYESSRENTDLQQPSAEASPNFEITIGTTDSFNSLFPSTSVPALRVDPKQNSKWKPSF
human_5+3_corrected VKLHESSRHN--LQMPSSQLFP-----LTGTSNLLHSTFMPALTTVKSQNSKLTSPF
mouse_5_corrected

```

```

rat      WPEHKYQLKSYSETIEKGKRAVSMSPHLSLPEASTHSHWNTQKHAISKSVFDKKPGQNP
human_5+3_corrected  NAEYQFWHKPYSDIAEKGGKPEVSLATTGLSEATTIVSDWDGQNTKKSDFDKKPVQEA
mouse_5_corrected    -----

```

**SECRET**

[illegible]

[illegible]





Figure 17

MQKRGREVSCLLISLTAICLVVTPGSRVCPRRCACYPTEVHCTFRDLTSIPDGPANVER  
VNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLSQLQVLKMSYNKVQIIE  
KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQIF  
KTSFIKXLYLYDNFTSLPKEMVSSMPNLESYLHGNPWTCDCHLKWLSEWMQGNP  
(SEQ ID NO: 15)

Figure 18

MKVKGRGITCLLVSAVICLVATPGGKACPRRCACYPTEVHCTFRYLTSSIPDSIPPNVE  
RINLGYNLVRMLMETDFSGLTKELELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK  
LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL  
QIFKISFIKFLYLSDNFLTSLPQEMSYPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI  
KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS  
AFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFSTFL  
VCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYKYKQVAPKPEDIFTNIEADLR  
ADPSWLMQDQISLQLNRTATTFTSLQIQYSSDAQITLPRAEHRPVKHKWTMISRDNNTK  
LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM  
ADSFDTGVIYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDPCHSTGIP  
DASISWVIPGNNVLYQSSRDKKVLNNGTLRLQVTPKDQGYRCVAANPSGVDFLIFQV  
SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVKGHTSSTSKRH  
NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTV  
SPPPVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN  
YGTEFSPVVNSQILPPEPTDFKLSTAILTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLG  
ATEFQSDSDQMGRGREHFQSRPPITVRTMIKD VNVKMLSSTTNKLLLESVNSHQTSVREV  
SEPRHNNHFYSHTTQILSTSTFPSPHTAAHSQFPPIRNSTVNIPLFRRFGRQRKIGGRGRIIS  
PYRTPVLRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSLPRELTTATAALSFPSPAAP  
TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT  
SIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLGAIKPPMTIIATRFSRRKIPWQQNFV  
NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNLTT  
AHHTTTKTHNPGSLPTKKELFPPLNPMLPSIISKDSSTKSIISTQTAIPATTPTFPASVITYE  
TQTERSRAQTIQREQEPQKKNRTDPNISPQSSGFTTPTAMTPPALAFTHSPPENTTGISST  
ISFHSRTLNLTDVIEELAQASTQTLKSTIASSETTLSSKSHQSTTTRKASLDTPIPPFLSSSAT  
LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLMQMPSSQLEPLTSSTSNLL  
HSTPMPALTTVKSQNSKLTPSPWAEQFWHKPYSDIAEKGGKPEVSMMLATTGLSEATTLV  
SDWDGQKNLTKKSDFDKPPVQEATTSKLLPFDLSRYIFEKPRIVGGKAASFTIPANSDAF  
LPCEAVGNPLPTIHWTRVSGDLNRSRGNQNSRVQVLPNGTSLIQRVEIQDRFQYLCASNL  
FGTDHLHVTLVSVSYPPRILERRTEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSE  
SSQGSRAVVTVDGTLVLHNLISIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRR  
QVIVGTWGESLKLPCAKGTPQPSVYVWVLSDGTEVKPLQFTNSKLFLLSNGTLYIRNLAS

SDRFTYECIATSSSTGSERRVVMLTMEERVTSPIEAASQKRTEVNFGDKLLLNC SATGEP  
 KPQIMRLPSKAVVDQGSWIHYPNGSLFIGVTEKDSGVYLCVARNKMGDDLILMHVSLR  
 LKPAKIDHKQYFRKQVLHGKDFQVDCKASGSPVPEISWSLPDGTMINNAMQADDSGHR  
 TRRYRLFNNGTLYFNKVGVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTN  
 KRIKAGDTAAVLDC EVTGD PKPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSG  
 EYVCVARNPSGDDTKMYKLDVVSKPPLINGLYTNRTVIKATAVRHSKKHFD CRAEGTP  
 SPEVMWIMP DNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFCVARNEGGE SVLVVQLE  
 VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSDGNPPPEI IWILPNGTRFSNGPQSY  
 QYLIASNGSFIISKTTREDAGKYRCAARNKVG YIEKL VILEIGQKPVILTYAPGTVKGISGE  
 SLSLHC VSDGIPKPNIKWTMPSGYVVD RPQINGKYILHDNGTLVIKEATA YDRGNYICKA  
 QNSVGHTLITVPVMIVA YPPRITNRPPRSIVTRTGAA FQLHCVALGVPKPEITWEMPDHS  
 LLSTASKERTHGSEQLHLQGTLVIQN PQTS DSGIYKCTAKNPLGSDYAATYIQVI (SEQ ID  
 NO: 16)

Figure 19

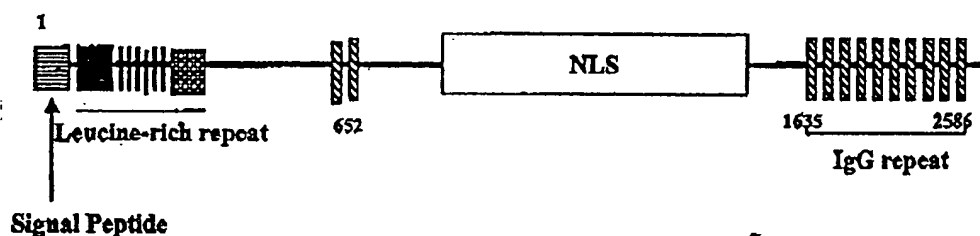


Figure 20

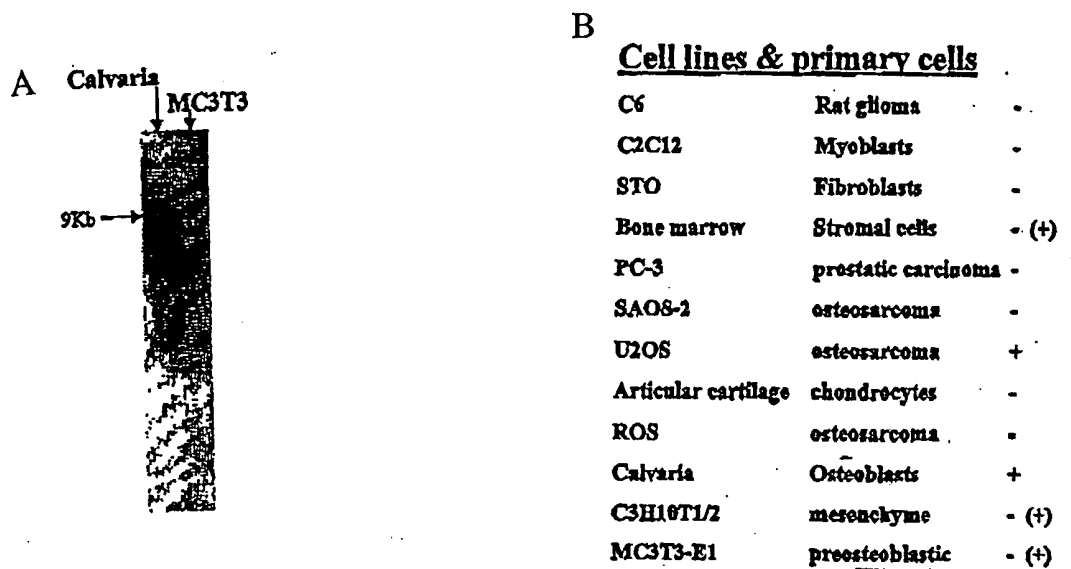


Figure 21

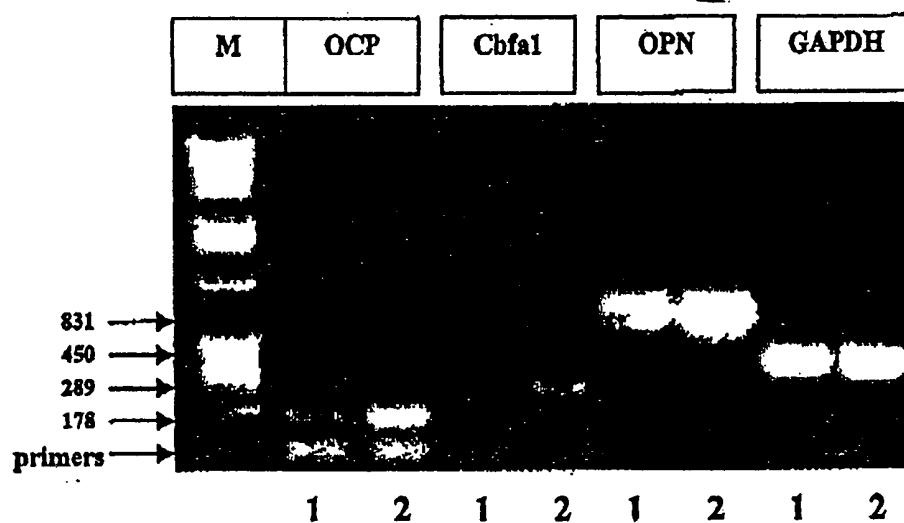


Figure 22

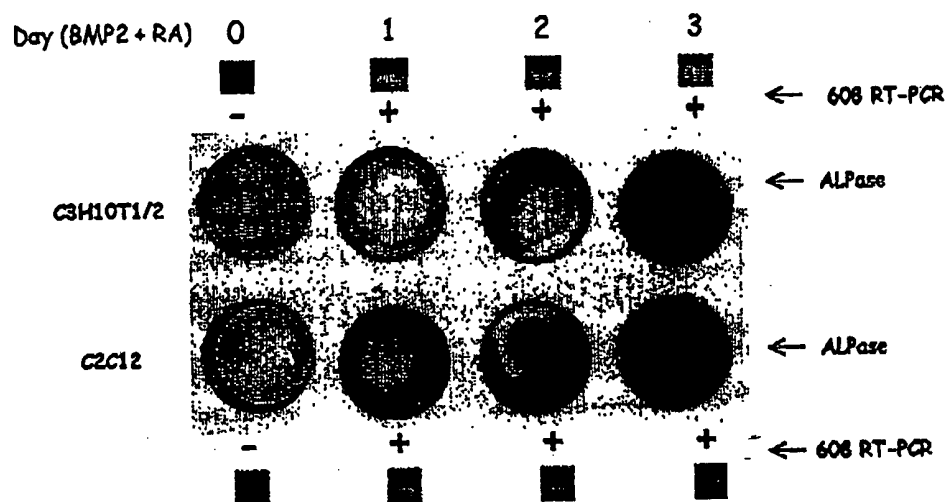
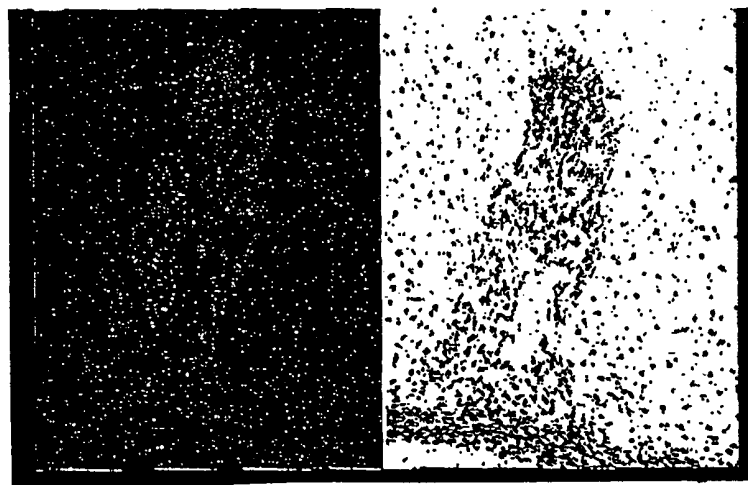


Figure 23



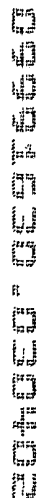
[illegible]

Figure 25

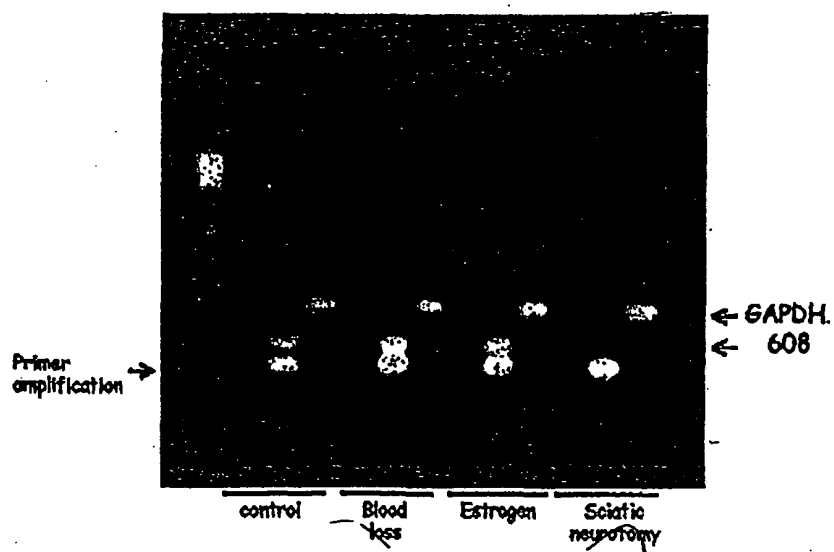


Figure 26

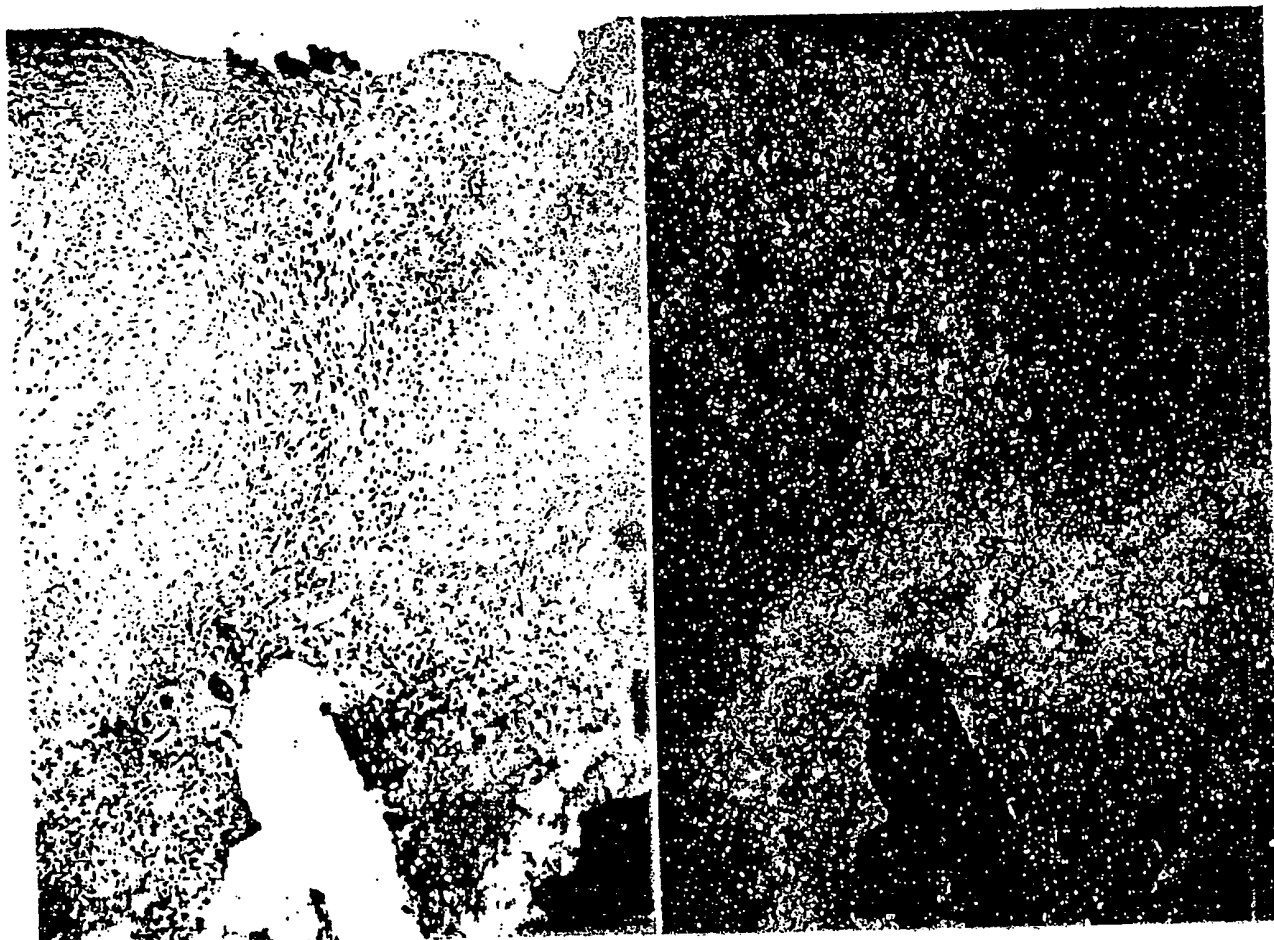


20140901 09:46:30

Figure 27

A

B



204000-000000



\_\_\_\_\_

A high-contrast, black and white photograph of a textured surface, possibly a rock or concrete. The image is characterized by a vertical crack running down the center. To the right of the crack, there is a dark, irregular shape that appears to be a shadow or a hole. The overall texture is rough and granular.

This is a high-contrast, black and white image showing a dense, textured surface. The image is characterized by a heavy, grainy texture with a large, bright, irregularly shaped area on the left side, which appears to be a reflection or a highlight. The rest of the image is predominantly black with scattered white specks and noise, suggesting a very dark or underexposed scene. There are no discernible figures, objects, or text.

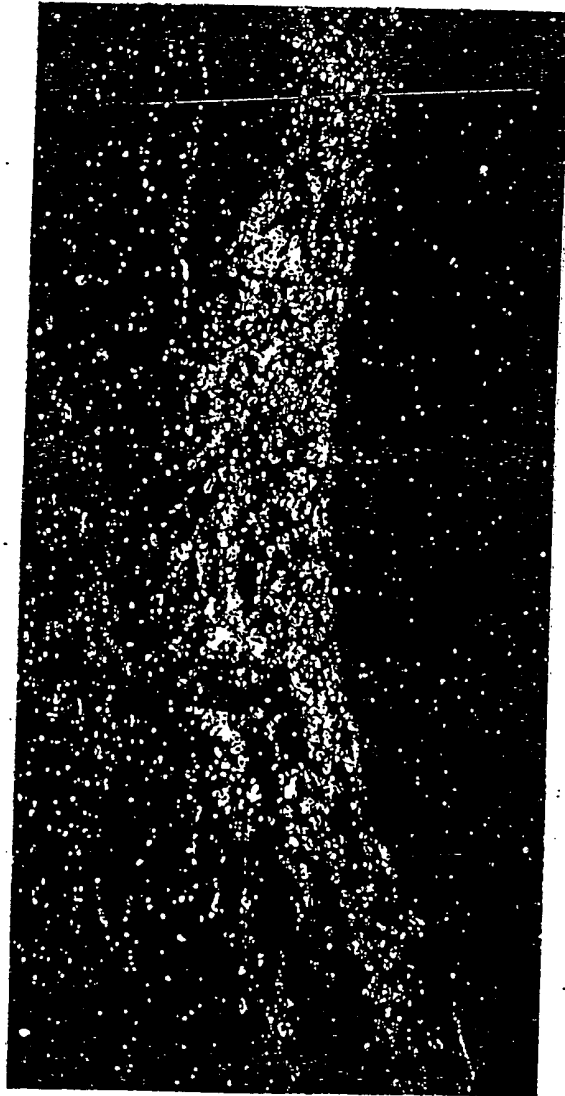
NAME	AGE	SEX	REL.	DATE	TIME	PLACE	REMARKS
JOHN	25	M	SON	1914	11	11	11
MARY	22	F	DAUGHTER	1914	11	11	11
JOHN	20	M	SON	1914	11	11	11
MARY	18	F	DAUGHTER	1914	11	11	11
JOHN	15	M	SON	1914	11	11	11
MARY	12	F	DAUGHTER	1914	11	11	11
JOHN	10	M	SON	1914	11	11	11
MARY	8	F	DAUGHTER	1914	11	11	11
JOHN	5	M	SON	1914	11	11	11
MARY	3	F	DAUGHTER	1914	11	11	11

Figure 29

A

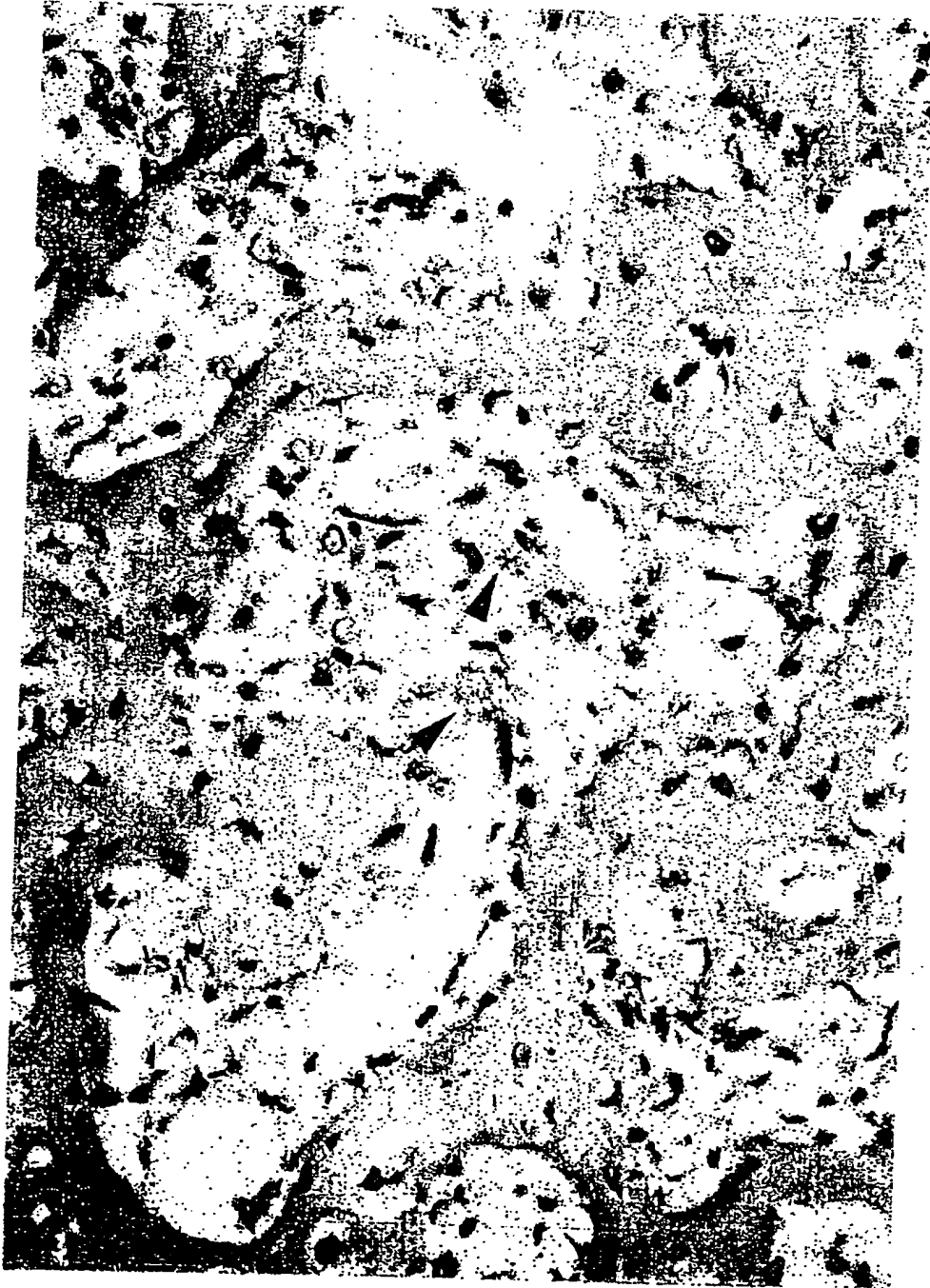


B



00001030 030402

Figure 30



00004630.030402

Figure 31



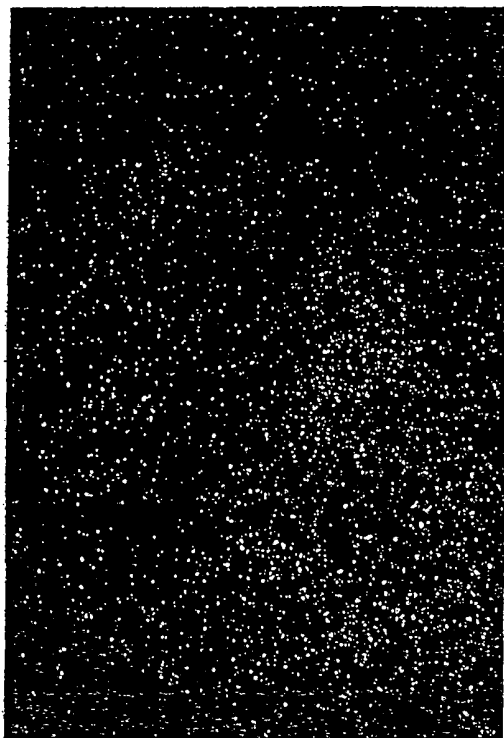
00001630.030402

Figure 32

A



B



204000-0001550

This image is a high-contrast, black-and-white scan of a textured surface. It appears to be a microscopic view of a material or a heavily degraded document page. The background is a light, grainy white, and it is covered with a dense distribution of small, dark, irregular specks and fibers. These dark elements vary in size and shape, some appearing as thin, elongated fibers and others as small, rounded or angular particles. The overall effect is one of a granular or fibrous structure. There are no discernible patterns, text, or other features that would allow for a more specific identification of the material.

Variable	Mean	SD	Median	Mode	Range	Skewness	Kurtosis
Age	35.2	12.5	32.0	30.0	20-55	0.15	3.2
Gender	1.2	0.4	1.0	1.0	1-2	-0.1	3.0
Education	12.5	2.1	12.0	12.0	9-15	0.05	3.1
Income	4500	1500	4000	4000	3000-7000	0.2	3.3
Marital Status	1.5	0.5	1.0	1.0	1-2	-0.1	3.0
Occupation	2.5	1.2	2.0	2.0	1-4	0.1	3.2
Health Status	1.8	0.6	1.5	1.5	1-2	-0.1	3.0
Stress Level	3.2	1.1	3.0	3.0	2-4	0.1	3.2
Life Satisfaction	4.5	0.8	4.0	4.0	3-5	-0.1	3.0
Resilience Score	2.8	0.9	2.5	2.5	2-4	0.1	3.2
Emotional Stability	3.5	1.0	3.0	3.0	2-4	0.1	3.2
Social Support	3.8	1.2	3.5	3.5	2-5	0.1	3.2
Work-Life Balance	3.0	1.1	2.5	2.5	2-4	0.1	3.2
Financial Stability	3.2	1.0	3.0	3.0	2-4	0.1	3.2
Physical Health	3.5	1.1	3.0	3.0	2-4	0.1	3.2
Mental Health	3.0	1.0	2.5	2.5	2-4	0.1	3.2
Overall Well-being	3.8	1.2	3.5	3.5	2-5	0.1	3.2

Figure 34

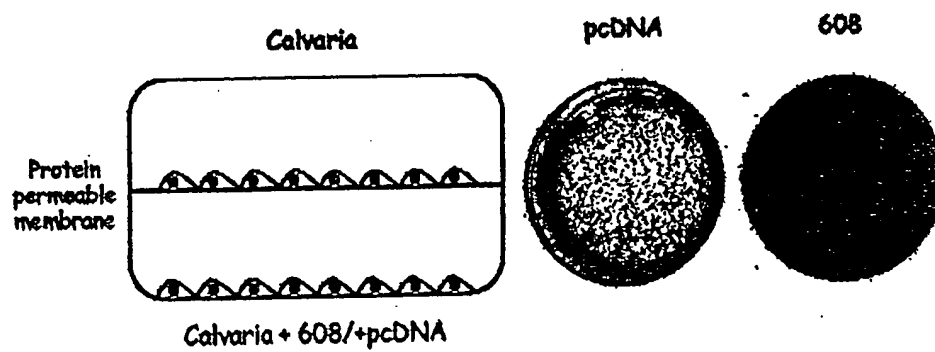


Figure 35

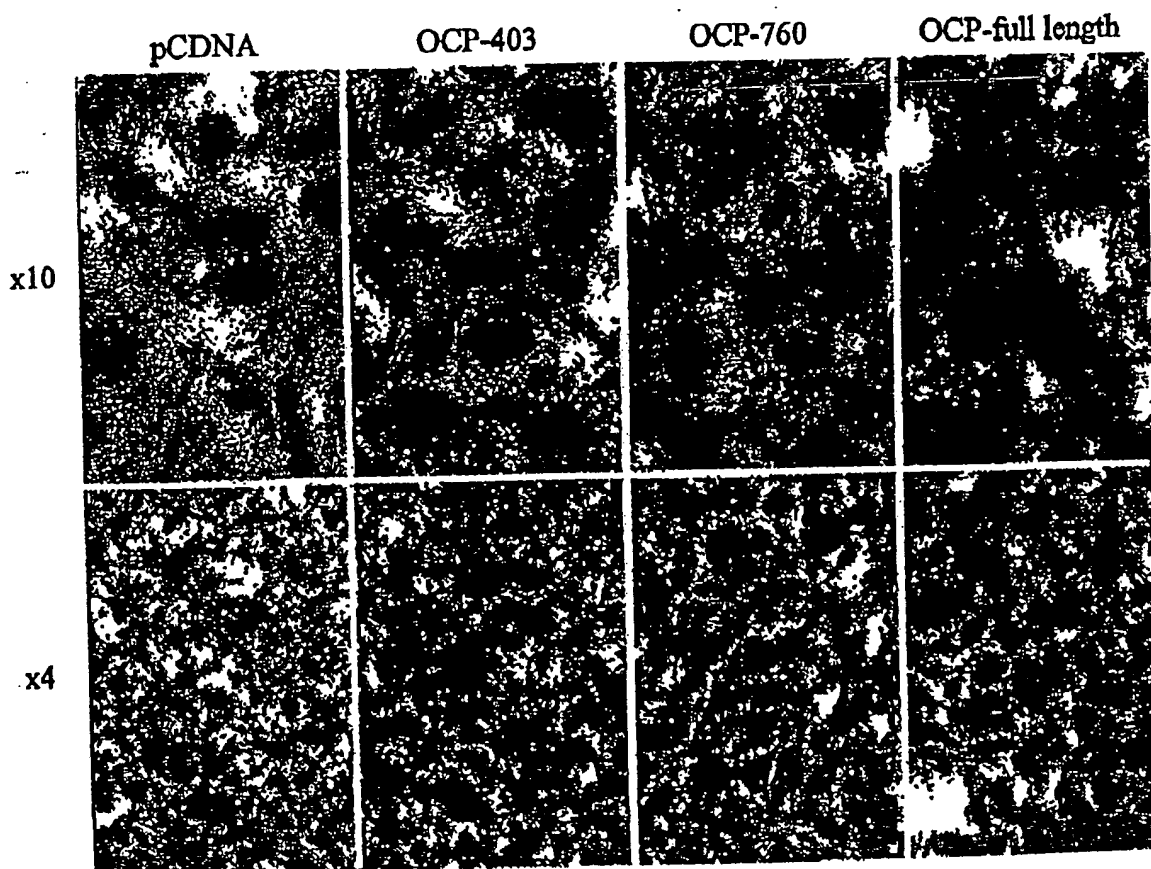


Figure 36

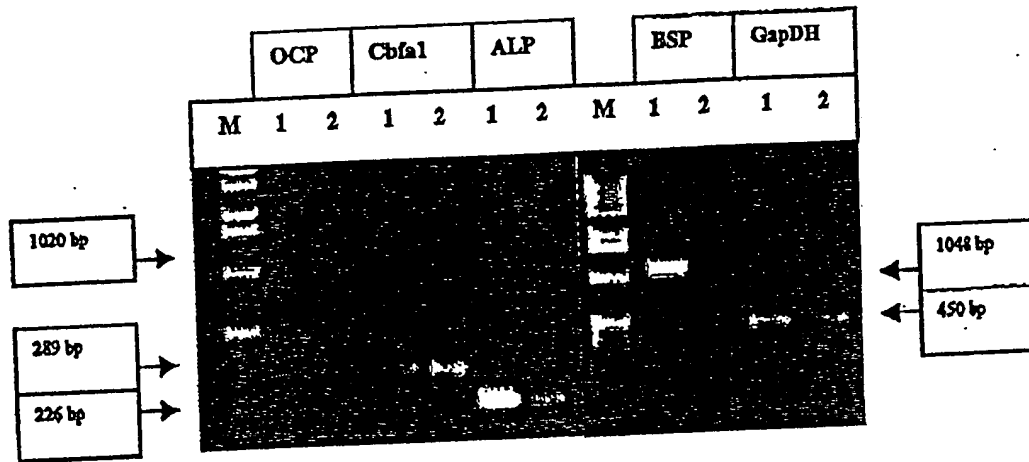


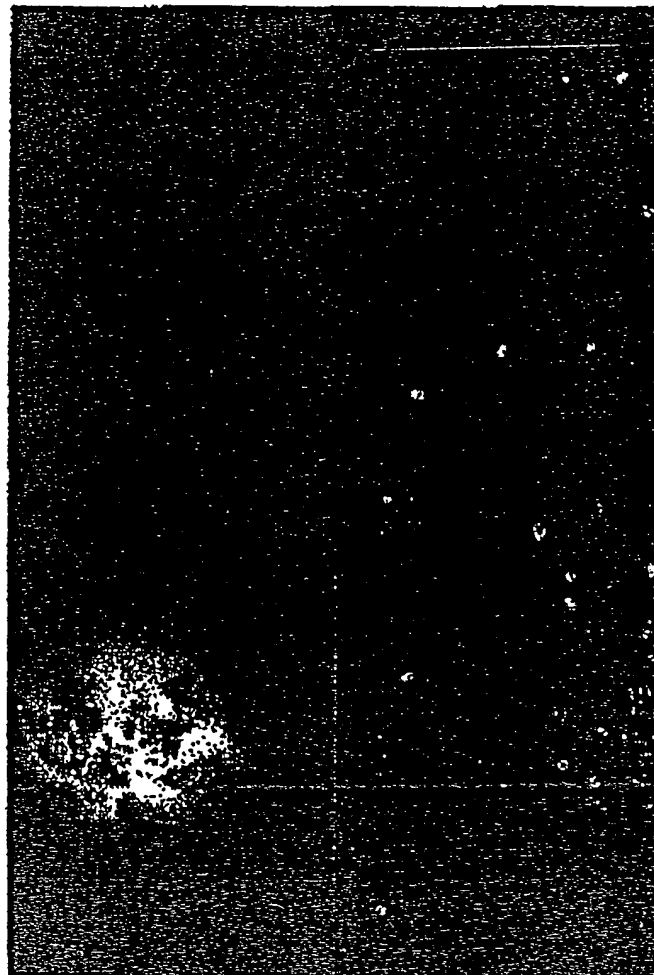
Figure 37

x 4

x 10

pCDNA  
ROS stable line

OCP  
ROS stable line





0994630-034462

Figure 38

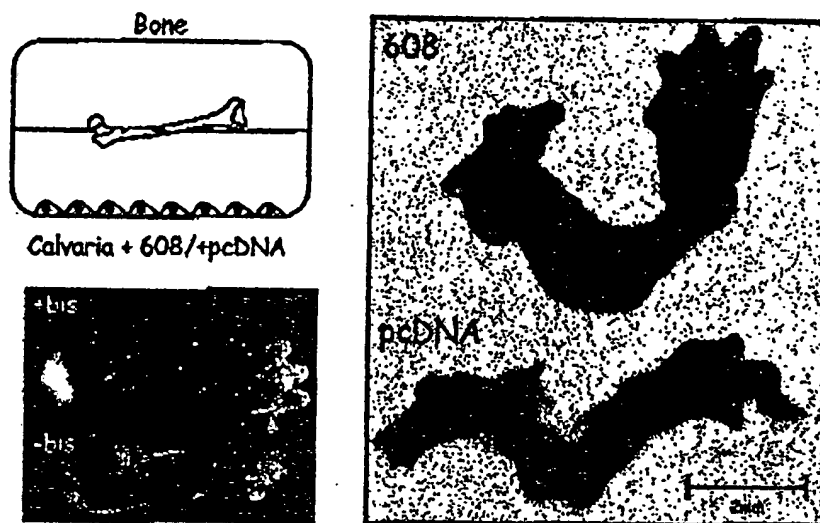


Figure 39

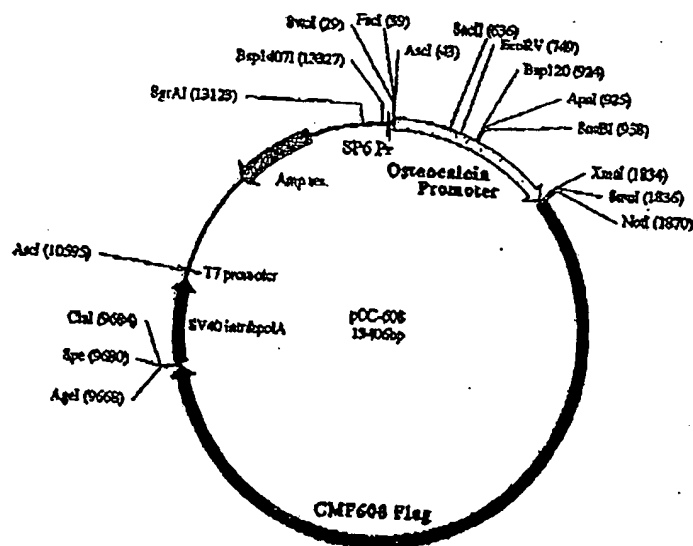
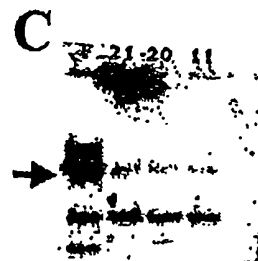
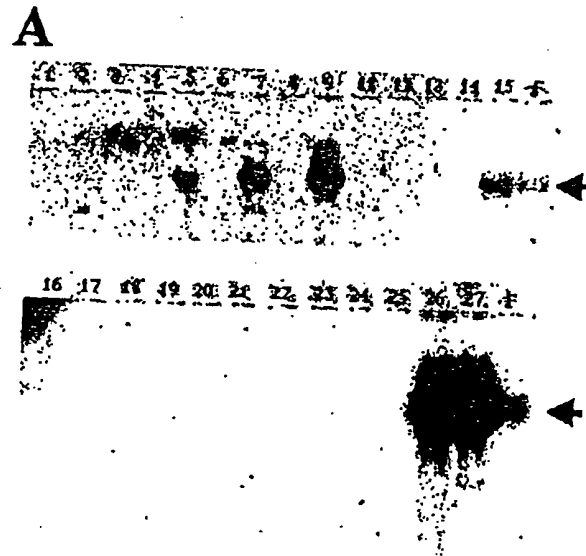


Figure 40



204050 0206520

Figure 41

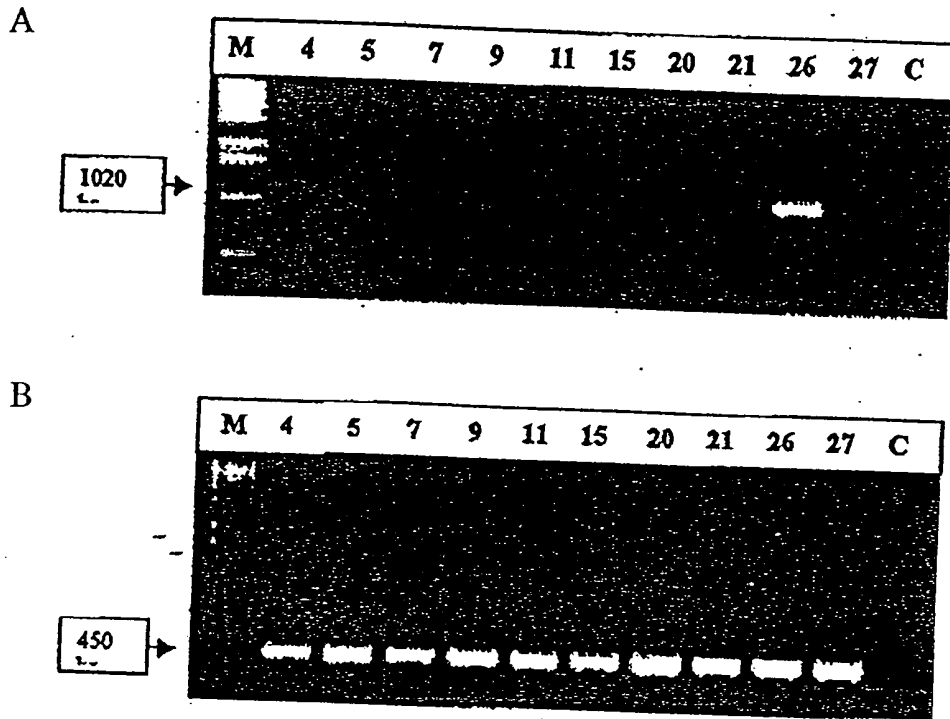
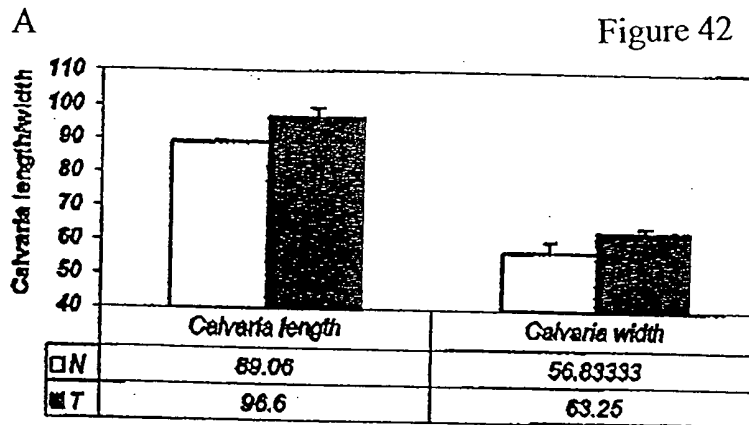
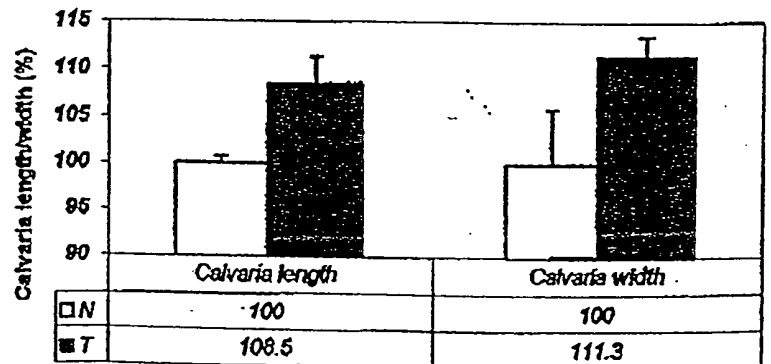


Figure 42



B



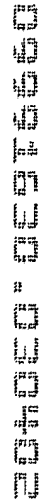
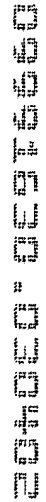
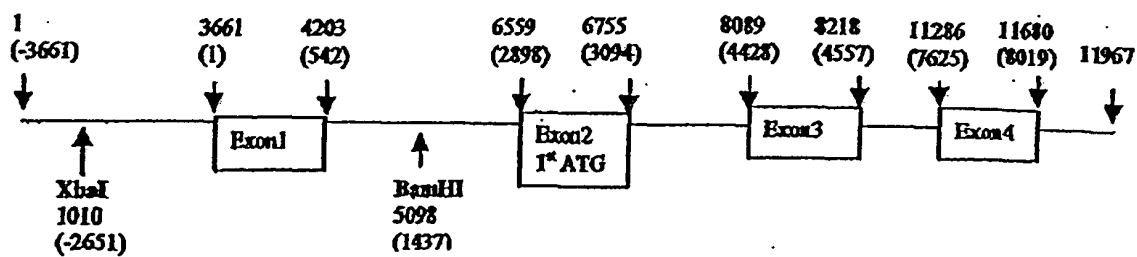
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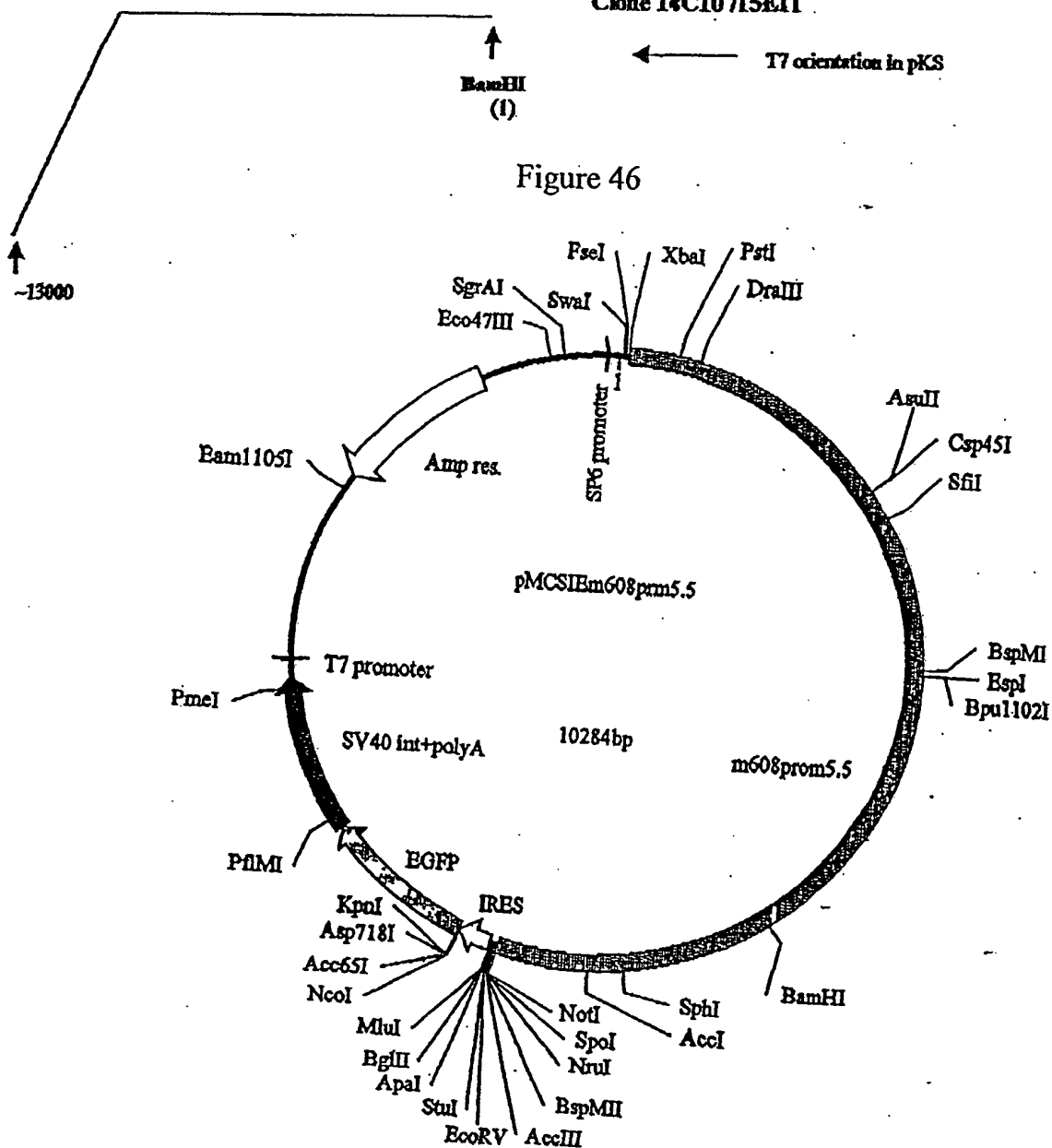
Figure 45



Clone 14C10 /15E11

T7 orientation in pKS

Figure 46



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Figure 48

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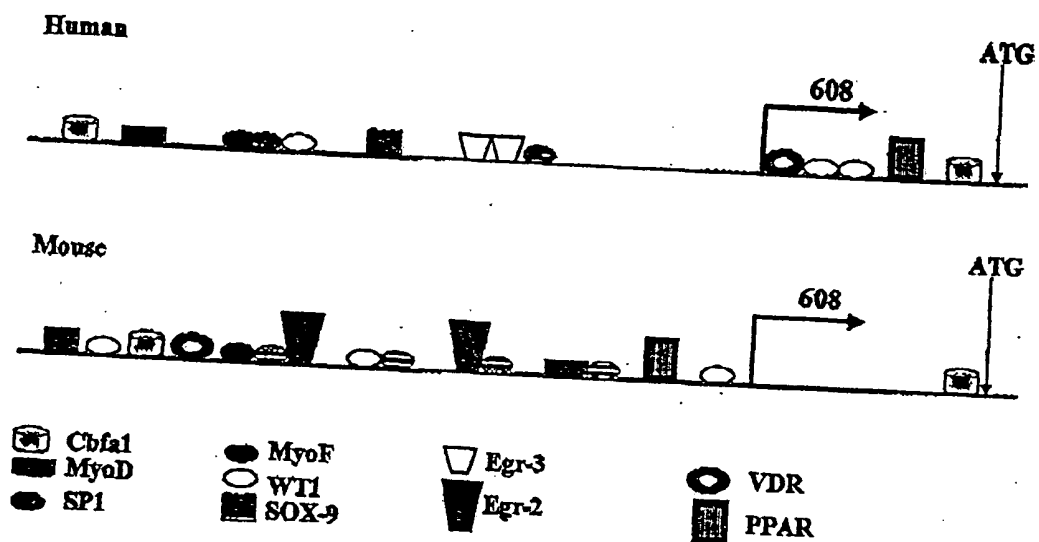


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(SEQ ID NO:18)

Figure 49



204000-000000





204500 000000

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 CTTCATAAGC GTCCATAGGA TATCTGAGGA ACATTCATCA AAAATAAGCC  
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 AACCTGCTGC AGTTTTTACA TGATAGACTT TGTTCCAGAT TGACAAGTCA  
 TCTTTCAGTT ATTTCTCTG TCACTTCAAA ACTCCAGCTT GCCCAATAAG  
 GATTTAGAAC CAGAGTGACT GATATATATA TATATATTTT AATTCAGAGT  
 TACATACATA CAGCTACCAT TTTATATGAA AAAAGAAAAA CATTTCTTCC  
 TGGAATCAGC TTTTATATA ATGTTTTATA TATATATTTT TTCCTTTCAA  
 ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGTCTT ATTAAAATTA  
 ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA  
 ATATAATTTT AAAAAATTTT TCTCCAACCT CTTCAAATT CAGTCACCAC  
 TGTTATATTA CTTTCTCCAG GAACCCTCCA GTGGGGAAGG CTGCGATATT  
 AGATTTCCCT GTATGCAAAG TTTTGTGGA AAGCTGTGCT CAGAGGAGGT  
 GAGAGGAGAG GAAGGAGAAA ACTGCATCAT AACTTTACAG AATTGAATCT  
 AGAGTCTTCC CCGAAAAGCC CAGAACTTC TCTGCAGTAT CTGGCTTGTC  
 CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC  
 CCATGAATAA TACACGACCT GTTATTTCCA TGAAGCTTT ACTGTATTTT  
 TAAGGTCAAT ATACTGTACA TTTGATAATA AAATAATATT CTCCAAAAA AAAAA

Figure 53

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGGCTGCTCCTTTGGCTGTGATCTGCCTGGTCGCCACC  
CCTGGGGGCAAGGCCTGTCTCGCCGCTGTGCCTGTTATATGCCTACGGAGGTACACTGCACATTTTCGG  
TACCTGACTTCCATCCCAGACAGCATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAACAGCTTG  
GTTAGATTGATGGAAACAGATTTTCTGGCCTGACCAAACTGGAGTTACTCATGCTTCACAGCAATGGC  
ATTCACACAATCCCTGACAAGACCTTCTCAGATTTGCAGGCCTTGCAGGTCTTAAAAATGAGCTATAAT  
AAAGTCCGAAAACCTTCAGAAAAGATACTTTTATGGCCTCAGGAGCTTGACACGATTGCACATGGACCAC  
ACAATATTGAGTTTATAAAACCCAGAGGTTTTTATGGGCTCAACTTTCTCCGCTGGTGCACTTGGAA  
GGAAATCAGCTCACTAAGCTCCACCCAGATACATTTGTCTCTTTGAGCTACCTCCAGATATTTAAATC  
TCTTTCATTAAGTTCTTACTTGTCTGATAACTTCTGACCTCCCTCCCTCAAGAGATGGTCTCCTAT  
ATGCCTGACCTAGACAGCCTTTACCTGTCATGGAAACCCATGGACCTGTGATTGCCATTTAAAGTGGTTG  
TCTGACTGGATACAGGAGAGCCAGATGTAATAAAATGCAAAAAGATAGAAGTCCCTCTAGTGCTCAG  
CAGTGTCCACTTTGTCATGAACCTTAGGACTTCTAAAGGCAAGCCGTTAGCTATGGTCTCAGCTGCAGCT  
TTCCAGTGTGCCAAGCCAACCATTGACTCATCCCTGAAATCAAAGAGCCTGACTATTCTGGAAGACAGT  
AGTTCTGCTTTCATCTCTCCCAAGGTTTTCATGGCACCCCTTTGGCTCCCTCACTTTGAATATGACAGAT  
CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAAGCCCTCAAGGACATCACCCATTGCATTTC  
ACTGAAGAAAATGACTACATCGTGCTAAATACTTCAATTTTCAACATTTTGGTGTGCAACATAGATTAC  
GGTCACATTTCAGCCAGTGTGGCAAATTTTGGCTTTGTACAGTGATTCTCCTCTGATAC TAGAAAGGAGC  
CACTTGCTTAGTGAAACACCGCAGCTCTATTACAAATATAAACAGGTGGCTCCTAAGCCTGAAGACATT  
TTTACCAACATAGAGGCAGATCTCAGAGCAGATCCCTCTTGGTTAATGCAAGACCAAAATTTCTTGCAG  
CTGAACAGAACTGCCACCACATTCAGTACATTACAGATCCAGTACTCCAGTGATGCTCAAATCACTTTA  
CCAAGAGCAGAGATGAGGCCAGTGAAACACAAATGGACTATGATTTCAAGGGATAACAATACTAAGCTG  
GAACATACTGTCTTGGTAGGTGGAACCGTTGGCCTGAACTGCCCAGGCCAAGGAGACCCACCCACAC  
GTGGATTGGCTTCTAGCTGATGGAAGTAAAGTGAGAGCCCCCTTATGTCAGTGAGGATGGACGGATCCTA  
ATAGACAAAAGTGGAAAATTGGAACCTCAGATGGCTGATAGTTTTGACACAGGCGTATATCACTGTATA  
AGCAGCAATTATGATGATGAGATATTCTCACCTATAGGATAACTGTGGTAGAACCTTTGGTTCGAAGCC  
TATCAGGAAAATGGGATTCATCACACAGTTTTTCATTGGTGAACACTTGATCTTCCATGCCATTCTACT  
GGTATCCCAGATGCCTCTATTAGCTGGGTTATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGAC  
AAGAAAGTCTAAACAATGGCACAATTAGAATATTACAGGTCACCCCGAAAGACCAAGGTTATTATTCGC  
TGTGTGGCAGCCAAACCCATCAGGGGTTGATTTTGTATTTTCCAAGTTTCAGTCAAGATGAAAGGACAA  
AGGCCCTTGGAGCATGATGGAGAAACAGAGGGATCTGGACTTGATGAGTCCAATCCTATTGCTCATCTT  
AAGGAGCCACCAGGTGCACAACCTCCGTACATCTGCTCTGATGGAGGCTGAGGTTGGAAAAACACCTCA  
AGCACAAAGTAAGAGGCACAACCTATCGGGAATTAACACTCCAGCGACGTGGAGATTCAACACATCGACGT  
TTTAGGGAGAATAGGAGGCATTTCCCTCCCTCTGCTAGGAGAATTGACCCACAACATTGGGCGGCAGT  
TTGGAGAAAGCTAAAAAGATGCTATGCCAGACAAGCGAGAAAATACCACAGTGAGCCACCCCAAGT  
GTCACCCAACTCCCAAACATACCTGGTGAAGAAGACGATTCTCAGGCATGCTCGCTCTACATGAGGAA  
TTTATGGTCCCGGCCACTAAAGCTTTGAACCTTCAGCAAGGACAGTGACTGCTGACTCCAGAACAATA  
TCTGATAGTCTTATGACAAACATAAATTATGGCACAGAATTCTCTCTGTTGTGAATTCAAAATACTA  
CCACCTGAAGAACCCACAGATTTCAAAGTGTCTACTGCTATTAAAACTACAGCCATGTCAAAGAATA  
AACCCAAACATGTCAAGCCAAATACAAGGCACAACCAATCAACATTCATCCACTGTCTTTCCACTGCTA  
CTTGGAGCAACTGAATTTCAAGACTCTGACCAGATGGGAAGAGGAAGAGAGCATTTCCAAAGTAGACCC  
CCAATAACAGTAAGGACTATGATCAAAGATGTCAATGTCAAATGCTTAGTAGCACCACCAACAACTA  
TTATTAGAGTCAGTAAATACCACAAATAGTCATCAGACATCTGTAAGAGAAGTGAGTGAACCCAGGCAC  
AATCACTTCTATTCTCACAATACTCAATACTTAGCACCTCCACGTTCCCTTCAGATCCACACAGCT  
GCTCATTTCTAGTTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGTTTCAGACGCTTTGGGAGG  
CAGAGGAAAATTGGCGGAAGGGGGCGGATTATCAGCCCATATAGAACTCCAGTTCTGCGACGGCATAGA  
TACAGCATTTTCAGGTCAACAACAGAGGTTCTTCTGAAAAAAGCACTACTGCATTCTCAGCCACAGTG  
CTCAATGTGACATGTCTGTCTGTCTTCCAGGAGAGGCTCACCCTGCCACAGCAGATTGTCTTTT  
CCAAGTGTCTGTCTCCCATCACTTCCCCAAAGCTGACATTGCTTAGAGTCCCATCAGAAGAGTCTACA  
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TATTTCAAGGACTGAAATTTCCCAAGTGACTCCAAGTGGTGCAGTCATGACATATGCTCCAACATCCATA  
CCCATGGAAAAAATCACAAGTAAACGCCAGTTACCCACGTGTGTCTAGCACCATGAAGCTAAAAGA  
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AGGTTTTCAGAAGGAAAATTCCTGGCAACAGAATTTGTAAATAACCATAACCEAAAAGGCAGATTA  
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CCACAGAGACAAAGTTCCCTTTCCATTTCAACACACTTTCAACAAGTGTGATGCAAAATCCATCTAAT  
ACCTTGACTACCGCTCACCACACTACGACCAAAACACAAATCCTGGAAGTCTTCCAACAAAGAAGGAG  
CTTCCCTTCCCACCCCTTAACCTATGCTTCTTAGTATTATAAGCAAGAGACTCAAGTACAAAAGCATC  
ATATCAACGCAACAGCAATACCAGCAACAACTCCTACCTTCCCTGCATCTGTCTCACTTATGAAACC  
CAAACAGAGAGATCTAGAGCACAACAATAACAAGAGAACAGGAGCCTCAAAGAAGAACAGGACTGAC  
CCAACATCTCTCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACACCTCTGCTCTGGCA





Figure 54

ORIGIN					
1	MKVKGRGITC	LLVSFAVICL	VATPGGKACP	RRCACYMPTE	VHCTFRYLTS
51	IPDSIPPNVE	RINLGYNLSV	RLMETDFSGL	TKLELLMLHS	NGIHTIPDKT
101	FSDLQALQVL	KMSYNKVRKL	QKDTFYGLRS	LTRLHMDHNN	IEFINPEVFX
151	GLNFLRLVHL	EGNQLTKLHP	DTFVSLSYLQ	IFKISFIKFL	YLSDFNLTSL
201	PQEMVSYMPD	LDSLYLHGNP	WTCDCHLKWL	SDWIOEKPDV	IKCKKDRSPS
251	SAQQCPLCMN	PRTSKGKPLA	MVSAAAFQCA	KPTIDSSLKS	KSLTILEDSS
301	SAFISPPQFM	APFGSLTLNM	TDQSGNEANM	VCSIQKPSRT	SPIAFTEEND
351	YIVLNTSFST	FLVCNIDYGH	IQPVWQILAL	YSDSPLILER	SHLLSETPQL
401	YYKYKQVAPK	PEDIFTNIEA	DLRADPSWLM	QDQISLQLNR	TATTFSTLQI
451	QYSSDAQITL	PRAEMRPVKH	KWTMISRDNM	TKLEHTVLVG	GTVGLNCPGQ
501	GDPTPHVDWL	LADGSKVRAP	YVSEDGRILI	DKSGKLELQM	ADSFDTGVYH
551	CISSNYDDAD	ILTYRITVVE	PLVEAYQENG	IHHTVFIGET	LDLPCBSTGI
601	PDASISWVIP	GNNVLYQSSR	DKKVLNNGTL	RILQVTPKDQ	GYRCAVANP
651	SGVDFLIFQV	SVKMKQQRPL	EHDGETEGSG	LDESNPJIAHL	KEPPGAQLRT
701	SALMEAEVGK	HTSSTSKRHN	YRELTQRRG	DSTHRRFREN	RRHFPSPARR
751	IDPQHWAAAL	EKAKKNAMPD	KRENTTVSPP	PVVTQLPNIP	GEEDDSSGML
801	ALHEEFMVPA	TKALNLPART	VTADSRITSD	SPMTNINYGT	EFSPVVNSQI
851	LPPEEPTDFK	LSTAIKTTAM	SKNINPTMSS	QIQGTTNQHS	STVFPLLLGA
901	TEFQSDSQMG	RGREHFQSRP	PITVRTMIKD	VNVKMLSSTT	NKLLLESVNT
951	TNSHQTSVRE	VSEPRHNHFX	SHTTQILSTS	TFFSDPHTAA	HSQFPPIRNS
1001	TVNIPLFRFR	GRQRKIGGRG	RIISPYRTPV	LRRHRSIFR	STTRGSSEKS
1051	TTAFSATVNL	VTCLSCLPRE	RLTTATAALS	FPSAAPITFP	KADIARVPSE
1101	ESTTLVQNPL	LLLENKPSVE	KTTPTIKYFR	TEISQVTPTG	AVMTYAPTSI
1151	PMEKTHKVNA	SYPRVSSSTNE	AKRDSVITSS	LSGAITKPPM	TIIAITRFSR
1201	RKIPWQQNFV	NNHNPKGRLR	NQHKVSLQKS	TAVMLPKTSP	ALPQRQSSPF
1251	HFTTLSTSVM	QIPSNTLTTA	HHTTTKTHNP	GSLPTKKELP	FPPLNPMPLS
1301	IISKDSSTKS	IISTQTAIPA	TTPTFPASVI	TYETQTERS	AQTIQREQEP
1351	QKKNRTDPNI	SPDQSSGFTT	PTAMTPPALA	FTHSPPENTT	GISSTISFHS
1401	RTLNLTDVIE	ELAQASTQTL	KSTIASSETTL	SSKSHQSTTT	RKASLDTPIP
1451	PFLSSSATLM	PVPISPFFTQ	RAVTDTRGDS	HFRLMTNTVV	KLHSSSRHNL
1501	QMPSSQLEPL	TSSTSNNLHS	TPMPALTTVK	SQNSKLTPSP	WAEYQFVHKP
1551	YSDIAEKGGK	PEVSMLATTG	LSEATTLVSD	WDGQKNTKKS	DFDKKPVQEA
1601	TTSKLLPFDS	LSRYIFEKPR	IVGGKAASFT	IPANSDAFLP	CEAVGNPLPT
1651	IHWTRVSGLD	LSRGNQNSRV	QVLPGNTLSI	QRVEIQDRGQ	YLCASANLFG
1701	TDHLHVTLSV	VSYPRIILER	RTKEITVHSG	STVELKCRAE	GRPSPTVTWI
1751	LANQTVVSES	SQGSRQAVVT	VDGTLVLHNL	SIYDRGFYKC	VASNPGGQDS
1801	LLVKIQVIAA	PPVILEQRRQ	VIVGTWGESL	KLPCTAKGTP	QPSVYVWLSD
1851	GTEVKPLQFT	NSKLFLFSNG	TLYIRNLASS	DRGTYECIAT	SSTGSERRVV
1901	MLTMEERVTS	PRIEASQKR	TEVNFGDKLL	LNCSATGEPK	PQIMWRLPSK
1951	AVVDQWSWIH	VYPNGSLFIG	SVTEKDSGVY	LCVARNKMGD	DLILMHVSLR
2001	LKPAKIDHKQ	YFRKQVLHGK	DFQVDCASG	SPVPEISWSL	PDGTMINNAM
2051	QADDSGHRTR	RYTLFNNGTL	YFNKVGVAAE	GDYTCYAQNT	LGKDEMKVHL
2101	TVITAAPRIR	QSNKTNKRIK	AGDTAVLDCE	VTGDPKPKIF	WLLPSNDMIS
2151	FSIDRYTFHA	NGSLTINKVK	LLDSGEYVCV	ARNPSGDDTK	MYKLDVVSKE
2201	PLINGLYTNR	TVIKATAVRH	SKKHFDCAE	GTPSPPEVMWI	MPDNIFLTAP
2251	YYGSRITVHK	NGTLEIRNVR	LSDSADFCV	ARNEGGEVSL	VVQLEVEML
2301	RRPTFRNPEN	EKIVAQLGKS	TALNCSVDGN	PPPELIWILP	NGTRFSNGPQ
2351	SYQYLIASNG	SFIISKTTRE	DAGKYRCAAR	NKVGYIEKLV	ILEIGQKPVI
2401	LTYAPGTVKG	ISGESLSLHC	VSDGIPKPNI	KWTMPSGYVV	DRPQINGKYI
2451	LHDNGTLVIK	EATAYDRGNY	ICKAQNVSCH	TLITVPVMIV	AYPPRITNRP
2501	PRSIIVTRGA	AFQLHCVALG	VPKPEITWEM	PDHSLSTAS	KERTHGSEQL
2551	HLQGTLVION	PQTSDSGIYK	CTAKNPLGSD	YAATYIQVI*	

2551 HLQGTLVION

**Figure 55**  
**OCP rat amino acid sequence**

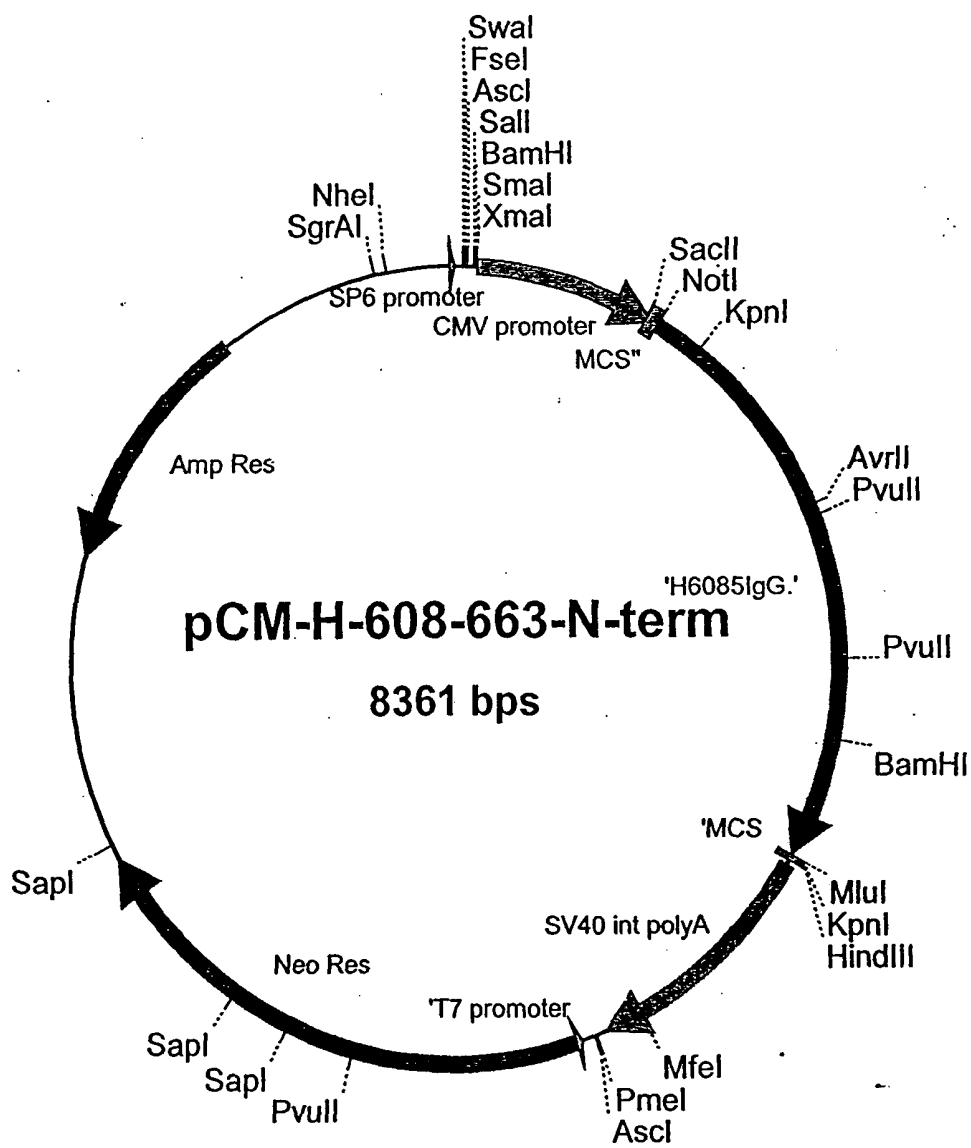
>608-663Nterm Rat Protein (663 aa)

MQVRGREVSGLLISLTAVCLVVTPGSRACPRRCACYVPTEVHCTFRYLTSIPDGIPANVE  
RINLGYNSLTRLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII  
RKDTFYGLGSLVRLHLDHNNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDTFVSLSYLQ  
IFKTSFIKYLFLSDNFLTSLPKEMVSYMPNLESYLHGPNWTCDCHLKWLSEWMQGNPDI  
IKCKKDRSSSSPQQCPLCMNPRISKGRPFAMVPSGAFLCTKPTIDPSLKSKSLVTQEDNG  
SASTSPQDFIEPFGSLSLNMTXXSGNKADMVCSIQKPSRTSPTAFTEENDYIMLNASFST  
NLVCSVDYNHIQPVWQLLALYSDSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEA  
DVRADPFWFQQEKIVLQLNRTATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNN  
PKLERTVLVGGTIALSCPGKGDPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQM  
ADSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTGV  
PDASISWILPGNTVFSQPSRDRQILNNGTLRILQVTPKQGHYQCVAANPSGADFSSFKV  
SVQ

608-663Nterm Rat Protein (663 aa)

Figure 56

# pCM-H-608-663-N-term



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